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## SUMMARIES

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Query Match 100.0%; Score 3071; DB 4; Best Local Similarity 100.0%; Pred. No. 2.1e-153; Matches 582; Conservative 0; Mismatches 0;

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Sequence 582

A,

The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

Claim 41; Page 168-172; 183pp; Japanese.

activity in cancer.

WPI; 2001-266143/27.

Nakamura

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Niwa بر :,

New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent

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## ALIGNMENTS

#### RESULT 1 AABB1987 ID AABB XX AABB AC AABB XX AABB XX Gang XX WO2( XX Gang XX WO2( XX W Hanai N, 30-SEP-1999; 99JP-00278291. 06-APR-2000; 2000JP-00105088. 29-SEP-2000; 2000WO-JP006774. Synthetic. cancer. Ganglioside; GD3; complementarity determining region; CDR; antibody; Ganglioside 03-JUL-2001 05-APR-2001. WO200123432-A1. AAB81987; AAB81987 standard; protein; (KYOW ) KYOWA HAKKO KOGYO KK. Shitara K, GB3 (first entry) specific antibody related protein SEQ ID NO: 582 AA.

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RESULT 2
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type complementation-determining region-transplanted antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a monoclonal antibody which can react specifically with ganglioside Gold. The antibody and its derivatives as useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplificat:
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IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
                                                                                                                                          TKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWO
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RESULT 3
AAB83156
IID AAB8
XX AAB8
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          Unidentified
                                                    Ganglioside
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                               Ganglioside;
                                                                         02-JUL-2001
                                                     GM2
                                GM2;
                                                                        (first
                                                    antibody-related
                               antibody;
                                                                                                                 protein;
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                               cytostatic; cytotoxic;
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cancer

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IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

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RESULT 4
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Best Local Similarity
Matches 526; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to derivatives of an antibody against ganglioside GM2. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 583 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibodies against ganglioside GM2 combined with drugs, radioisotopes or proteins for treatment and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1999;
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                                              INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
                                                                                                        NNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISN
                                                                                                                                                     RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGI
                                                                                                                                                                                                     DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                               SSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
                                                                                                                                                                                                                                                                                                                                                                                          SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                        NOKEKSKVTITVDTSTSTAYMELHSLRSEDTAVYYC--ATYGHYYGYMFAYWGQGTLVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY
                                                                                                                                         RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGI
                                                                                                                                                                                      DELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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                                                                                            NNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2780.5; DB 4;
Pred. No. 3.9e-138;
2; Mismatches 32;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. tumors, has lo
activity in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human type complementation-determining domain transplanted antibody and derivatives against ganglioside GD2, useful in diagnosis and therapy of e.g. tumors, has low antigenicity, little side effects but potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ganglioside; GD2; mouse; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3;
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TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRMQ
                                                       TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                        SVFLFPPXPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                       SVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                                                      LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
                                                                                                                                                                                          STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
                                                                                                                                                                                                         STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
                                                                                                                                                                                                                                            NSALMSRLTISKDNSKNOVFLKMSSLTAADTAVYYCAKRSDDYSWFAYWGOGTLVTVSSA
                                                                                                                                                                                                                                                           QVQLQESGPGLVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGS-TNY
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                                                                                                                                         LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 111-114; 123pp; Japanese
                                                                                                                                                                                                                                                                                                                                              89.9%;
ilarity 90.0%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                              22;
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                                                                                                                                                                                                                                                                                                                                              Score 2760.5; DB 4;
Pred. No. 4.3e-137;
2; Mismatches 35;
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                                                                                                          Query Match
Best Local Similarity
Matches 516; Conserv
                                                                                                                                                                                       The present invention relates to novel recombinant anti-EpCAM (human epithelial cell adhesion molecule) antibodies comprising an amino acid sequence defining an immunoglobulin light or heavy chain framework region. Sequences of the present invention are useful for the diagnosis, prognosis and treatment of cancer. They are also used in gene therapy. The present sequence is KS antibody heavy chain-interleukin 2 (II-2) fusion protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                               Sequence 579
                                                                                                                                                                                                                                                                                                                                      New recombinant anti-EpCAM antibody having an amino acid sequence defining an immunoglobulin light or heavy chain framework region, for the diagnosis, prognosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                              Disclosure; Page 80-82; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin; diagnosis; epithelial cell adhesion molecule;
cancer; gene therapy; interleukin-2; IL2; fusion protein.
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                                                                   EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY
                   SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYYFDSWGQGTLLTVSS
                                                   ADDFKGRFAFSLETSTSTAFLQINNLRSEDTATYFCVRFISKGDY---
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                                                                                                         89.6%; Score 2750.5; DB 6; 88.5%; Pred. No. 1.4e-136; tive 32; Mismatches 30;
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                                                                                             New fusion protein comprising a non-IL-2 moiety fused to moiety, useful for preparing a composition for treating infections or immune disorders.
                                                                                                                                                                                                                                                 Gillies
                                                                                                                                                                                                                                                                                                                                            04-DEC-2001;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dI-KS-ala-IL2
                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2002; 2002WO-US038780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Unidentified.
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                                                                                                                                                                                                                                                                                                 LEXIGEN
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2002US-0371966P.
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Ig; fusion protein; human.
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                                                                                                                    o a mutant IL-2 cancer, viral
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Example 10; Page 60-63;

71pp; English.

invention relates to cytokine fusion proteins with increased

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Best Loc
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            WO2004055056-A1
                                                                  immunoglobulin;
                                                                                         Humanised
                                                                                                                                                           ADP42961
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                                                                                                                                                                                                                 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
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                                                                                       immunoglobulin heavy chain-IL-2 fusion
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                                                         <u>Burface</u>
                                                                                                             (first
                                                      variable region; antibody; GD2;
rface glycosphingolipid; IL-2.
                                                                                                                                                          protein;
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Pred. No. 1.4e-136;
12; Mismatches 30;
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The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody mabe used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such a cancer. The present sequence represents an immunoglobulin heavy chain-IL 2 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified m14.18 antibodies with reduced immunogenicity specifically bind the human cell surface glycosphingolipid for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004-488049/46.
DB; ADP42959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERCK PATENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTCPPCPAPELLGGP
LYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVBPKSCDKTHTCPPCPAPELLGGP
                         KNPKLTRMLTFKFYMPKKATELKHLQCLEBELKPLEEVLNLAQSKNFHLRPRDLISNINV
                                                                                                            QGNVFSCSVMHEALHNHYTQKSLSLSFGKAPTSSSTKKTQLQLEHLLLLDLQMILMGINNY
                                                                                                                                                                            TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                                                                                      TKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                                                                                                                                                  TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
                                                                                                                                                                                                                                                                                         TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                                                                                                                                       STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMMVRQNIGKSLEWIGAIDPYYGGTSY
KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV
                                                                                       QGNVFSCSVMHEALHNHYTQKSLSLSPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.6%; ilarity 89.0%; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2719.5; DB 8
Pred. No. 6.1e-135;
4; Mismatches 33;
                                                                                     APTSSSTKKTQLQLEHLLLDLQMILNGINNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GMEY---WGQGTSVTVSSA
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RESULT 8
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Best Local S
Matches 500
                                                                                                                                                                                                                                                                                                                                     The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion proteins. The fusion protein comprises a non-interleukin-2 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is dI-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising dI-KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2 moiety, useful for preparing a composition for treating cancer, viral infections or immune disorders.
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12-APR-2002;
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                                                                                                                                                                                                                                                                                                             Sequence 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2002; 2002WO-US038780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-513757/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy;
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                                                                                   118
 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Page 68-71; 71pp; English.
                                          GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                   YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSS
                                                                                                                                                                                                                   EVQLVESGGDFVQPGGSLRVSCAASGFAFSH-YAMSWVRQAPGKGLEWVAYISSGGSGTY
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                   ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                   ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                          YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGKWSK--FDYWGQGTLVTVSS
                                                                                                                                                                                               QVQLQESGPGLVKPSETLSLTCAVSGYS1SSGYYWGWIRQPPGKGLEWIGSIYHSGS-TY
                           GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (gamma4h)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-2; IL-2; cancer; viral infection; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEXIGEN
                                                                                                                                                                                                                                                       Conservative
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2002US-0371966P.
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                                                                                                                                                                                                                                                                                                             AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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                                                                                                                                                                                                                                                                   85.3%;
                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                     Score 2621; DI
Pred. No. 9.2e
29; Mismatches
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                                                                                                                                                                                                                                                                   DB 6;
.2e-130;
                                                                                                                                                                                                                                                                                Length 580;
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RESULT 9
AAOJ0913
AD AAOJ
XX AAOJ
AC AAOJ
XX AOJ
AC AAOJ
XX Qyto
XX Cyto
XX Cyto
XX Gyto
XX Homo
OS Unid
XX 12-J
XX 12
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                                                The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion proteins. The fusion protein comprises a non-interleukin-2 (IL-2) molety fused to a mutant IL-2 molety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is dI-NHS76 (gammazh) (FN>AQ)-ala-IL2 (D2OT) variant protein comprising dI-KS heavy chain fused to human IL-2 (D2OT) variant protein. This sequence is used to illustrate the method of the invention
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12-APR-2002;
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Sequence 580
                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2 moiety, useful for preparing a composition for treating cancer, viral
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Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
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                                                                                                          Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; applastic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersenssitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia.
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Pred. No. 4.4e-128;
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Query Match Best Local S Matches 426

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The present invention relates to novel antibodies that specifically bind covery late activation (VLA-1; betal containing integrins) antigens and complete containing integrins and complete containing these antibodies to treat immunological disorders. The conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. thinitis, respiratory distress syndrome, asthma, containing the conditions (e.g. inflammatory distress syndrome, asthma, containing the conditions (e.g. inflammatory bowel disease, Crohn's disease, contestinal conditions (e.g. inflammatory bowel disease, Crohn's disease, contains and colorectal cancer), complete containing the conditions (e.g. through bowel disease, repriatits, irritable bowel syndrome, colitis and colorectal cancer), complete containing the conditions (e.g. through bowel disease, repriatitis, aplastic anaemia, containing the conditions (e.g. through bowel disease, remaining the containing the conditions (e.g. atherosclerosis), thyroiditis, aplastic anaemia, containing the conditions (e.g. through bowel disease, remaining the conditions of the conditions 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, ecze burns, dermatitis, and abnormal proliferation of hair follicle cells o
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        to very late activation (VLA-1; betal containing integring) antigens and methods of using these antibodies to treat immunological disorders. The anti-VLA-1 antibodies are useful for preventing or treating VLA-1 mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, bronchitis, tendonitis, bursitis, fever, migraine headaches, gastrointestinal conditions (e.g. inflammatory bowel disease, Crohn's disease, gastritis, irritable bowel syndrome, colitis and colorectal cancer), vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia, periarteritis nodosa, Hodgkin's disease, myasthenia gravis, rheumatoid arthritis, systemic lupus erythematosus and multiple early irrital
                                                                                                                                                                                                                                                                                                                                                                                          New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; mutant; mutein.
                                                                                                                                                                                                                                                                         The present invention relates to novel antibodies that specifically bind
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Best Local Similarity
Matches 425; Conserv
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QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
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Pred. No. 6.8e
4; Mismatches
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5.8e-110;
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RESULT 12
AAO18400
13-OCT-2000;
13-MAR-2001;
21-JUN-2001;
                                                                                                                           Mus sp.
Synthetic.
                                                                                                         WO200230986-A2
                                                                                                                                                        Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer; neoplasia; LT-beta-R; light chain; heavy chain; variable region.
                                                                                                                                                                                       Mature humanised murine CBE11 heavy chain variable domain
                                                                                                                                                                                                           11-OCT-2002
                                                                                                                                                                                                                                                AAO18400 standard; protein; 449 AA
                                                                 12-OCT-2001; 2001WO-US032140.
                                                                                     18-APR-2002.
        BIOJ )
        BIOGEN INC
                          2000US-0240285P.
2001US-0275289P.
2001US-0299987P.
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sarcoidosis,

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Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periatteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQGNVFSCSVMHEALHNHYTQKSLSLSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYS!
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                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nction relates to humanised anti-lymphotoxin beta receptor bodies. These are derived from the murine LT-beta-R CBE11 and can be used to treat neoplasia in humans. The is a humanised murine CBE11 heavy chain variable region
                                                                                                                                                                                                                                                      chain mutant protein, hsAQC2.
                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                               entry)
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Pred. No. 8.7e-110;
3; Mismatches 18;
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systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failute; sarcoidosis; Behcet s syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; mutant; mutein.
                                                                                                                       13-APR-2001; 2001US-0283794P.
06-JUL-2001; 2001US-0303689P.
                                                                                                                                                                                                                        12-APR-2002;
                                                                                                                                                                                                                                                                                                                                             WO200283854-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis.
                                                             (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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EA,
   Saldanha
   Ä,
Karpusas
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mediated anti-VLA-1 antibodies are useful for preventing or treating VLA-1-iated immunological or inflammatory disorders, e.g. psoriasis, eczerns, dermatitis, and abnormal proliferation of hair follicle cells o

Example 23; Page 92; English

WPI; 2003-093009/08

CC to very late activation (VLA-1; betal containing integrins) antigens and CC methods of using these antibodies to treat immunological disorders. The CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-CC mediated immunological or inflammatory disorders such as skin related CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, CC bronchitis, tendonitis, respiratory bowel disease, Crohn's disease, CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease, CC astoliar diseases (e.g. atherseclerosis), thyroiditis, aplastic anaemia, CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, carbitritis, systemic lupus erythematosus and multiple sclerosis), renal CC authoritis, systemic lupus erythematosus and multiple sclerosis), renal CC dilure, sarcoidosis, naphrotic syndrome, Behcet's syndrome, gingivitis, CC upolymyositis, hypersensitivity, (e.g. delayed type hypersensitivity or CC compositis, hypersensitivity, graft and transplant rejections, graft CC upocardial ischaemia or endotoxin shock syndrome. The present sequence is conducated protein, hsAQC2 heavy chain mutant protein, hsAQC2 invention relates to novel antibodies that specifically bind

Sequence 447 æ

Similarity

72.8%;

.5; DB 6; l.1e-109;

Length

447;

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Matches 424
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                                                                                                         SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA
                                                                                                                                          EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY
                                                                                                                                                       EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY
                                               STKGPSVFPLAPSSKS
                                                                                             LDSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA
                                                                                                                                                                                       Conservative
                                               rsggtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlossg
                                                                                                                                                                                     Score 2236.5;
Pred. No. 1.1e
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RESULT 14
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            This sequence represents the heavy chain of a selected phage antibody against human OX40 receptor. OX40 receptor, family which is expressed on ACT-4, ACT3) is a member of the TNF receptor family which is expressed on activated CD4+ T cells. Triggering of this receptor enhances the proliferation of CD4+ memory cells. A human OX40 receptor specific phage antibody (scFv) represents the agonistic binding molecule of the invention which is capable of binding to and stimulating the human OX-40-receptor. The binding molecules of the invention are useful as a medicament for treating neoplastic, viral or bacterial disorder or disease, for stimulating T-cells in vitro and for enhancing the immune response in a human or animal against a tumour, bacterial on human which involves, administration to the human, where the modulating includes in the state of the human, where the modulating includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; OX40 receptor; specific phage antibody; scFv; CD134; ACT-4; ACT35; TNF receptor family; CD4+; T cell; tumour necrosis factor; proliferation; immune response; memory cell; tumour; bacterial; viral; antigen; leukaemia; neoplasm; bile duct carcinoma; bladder carcinoma; severe acute respiratory syndrome; SARS; herpes simplex virus; HSV; hepatitis B virus; HSV; HIV; Mycobacterium tuberculosis; Pseudomonas aeruginosa; Vibrio cholerae.
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 stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                         Bakker ABH,
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                                                                                                                                                                                                                                                                      4; SEQ ID NO 28; 148pp; English.
                                                                                                                                                                                                                                                                                                       agonistic binding molecule capable of binding to and stimulating OX-40-receptor, useful for modulating T-cell proliferation.
                                                                                                                                                                                                                                                                                                                                                             ADH34601.
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Best Local Similarity
Matches 420; Conserv
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                                                                                                                                 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                        SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                                                SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQS
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                WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                      EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                      SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                                 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                              NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE
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93.1%;
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Pred. No. 1.1e-109;
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Human; antibody; stem cell factor; mast cell growth factor; asthma; steel factor; c-kit ligand; gene therapy.
                                                                                               Human A2-G8 SCF antibody heavy chain variable and constant region
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                                                                                                                                                                                                                                                                                      AAO31101 standard;
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                                                                                                                                                                                                                                                                                   protein;
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RESULT 15
AAC31101
ID AAC311
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XX Human
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XX Homo
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XX 16-DE
XX 17-DE
XX 17-DE WO2003051311-A2 17-DEC-2001; 2001US-0342174P 16-DEC-2002; 2002WO-US040227. 26-JUN-2003. FARB ) BAYER CORP

Takeuchi T,

Tomkinson A,

Neben

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Best Local S
Matches 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain variable and constant
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified human antibody that binds to stem cell factor protein, useful for preparing a composition for treating asthma.
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            424 VFSCSVMHEALHNHYTQKSLSLSPGK 449
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                                              VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                             LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                             LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF 243
                                                                                                                                                                                                                                                                                          VKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSASTK 123
                                                                                                                                                              LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 303
                                                                                                                                                                                                                                             GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
                                                                                                                                                                                                                                                              GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 183
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                                                                                               VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
VFSCSVMHEALHNHYTQKSLSLSPGK
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Pred. No. 1.4e-109;
7; Mismatches 17;
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Search completed: December 23, 2004, 18:57:36 Job time : 160.692 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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    Score
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seq length: 2000000000
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
      GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-026-985-71
US-09-121-9528-71
US-09-234-340A-71
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US-08-466-1518-8
US-08-466-1518-8
US-08-887-5528-14
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US-09-109-207C-16
US-09-109-207C-16
US-09-109-207C-16
US-09-109-207C-16
US-09-296-005-14
US-09-296-005-14
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US-09-716-028-16
US-09-716-028-16
US-09-716-028-16
US-09-887-3528-18
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Sequence 71. Appl Sequence 71. Appl Sequence 71. Appl Sequence 71. Appl Sequence 72. Appli Sequence 8. Appli Sequence 8. Appli Sequence 8. Appli Sequence 14. Appli Sequence 16. Appl Sequence 17. Appl Sequence 18. Appl Sequence 2. Appli Sequence 2. Appli Sequence 2. Appli Sequence 2. Appli Sequence 18. Appli Sequence 18. Appli Sequence 2. Appli Sequence 18. Appli Sequence 1
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                                                                                ; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-71
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US-09-027-449-71
Query Match 71.5%; Sometime 71.5%; Sometime 90.9%; Properties 14; Conservative 14;
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Fr
STATE: California
                                                                                                                                                                                                                        TELEPHONE:
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Result No.

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ALIGNMENTS	US-08-378-939-10	US-09-485-737B-67	US-08-030-175-41	US-09-485-737B-90	US-08-030-175-42	US-08-458-516-13	US-09-383-916-8	US-09-526-098-8	US-08-487-550-8	US-09-304-465A-2	US-09-680-148-2	US-09-679-397-2	US-10-113-996-18	US-09-483-588-2	US-09-716-028-18	US-09-920-171-18	US-09-680-145-2	US-09-282-846-2
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### Sequence 71, Application US/09027449 Patent No. 6025158 GENERAL INFORMATION: COMPUTER: IBM PC COMPACTIBLE COMPUTER: IBM PC COMPACTION SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/027,449 FILING DATE: 20-Feb-1998 CLASSIFICATION UNBER: 60/074,330 APPLICATION NUMBER: 60/074,330 APPLICATION NUMBER: 60/074,330 FILING DATE: 22-Jan-1998 PRIOR APPLICATION NUMBER: 60/038,664 FILING DATE: 21-Feb-1997 ATTORNEY/AGENT INFORMATION: NAME: LOVE, Richard B. REGISTRATION NUMBER: 34,659 REFERENCE/DOCKET NUMBER: p1085R3-2 TELEPHONE: 60/025-5530 TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: APPLICANT: Leong, Steven R. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk Gonzalez, Tania R. Leong, Steven R. 650/225-5530 Genentech, Inc. Francisco P1085R3-2

Score 2194.5; DB 3; Pred. No. 2.3e-161; 4; Mismatches 24;

Length 452;

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Gaps

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STREET: 1 DNA Way
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MINPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIPTCATION:
APPLICATION INFORMATION:
NAME: LOVE, Richard B.
REGISTRAFION UMMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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US-09-026-985-71
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Patent No. 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geonzalez, Tania R.
APPLICANT: Geonzy, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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US-09-121-952A-71
; Sequence 71, Application US/09121952A; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Heei, APPLICANT: Koumenis, Iphigenia; APPLICANT: Leong, Steven R.; APPLICANT: Presta, Leonard G.; APPLICANT: Shahrokh, Zahra, APPLICANT: Shahrokh, Zahr
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Best Local S
Matches 411
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/121,952A

FILING DATE: 24-Jul-1998

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech Tra
                                                                                                                                                                                                                                                                                                                                                                                STREET: 1 DNA Way
CITY: South San Fra
STATE: California
COUNTRY: USA
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61 NQKFKGRFTLSRDNSKNTAYLOMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120
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: San Francisco
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90.9%; Pred. No. 2.30
ative 14; Mismatches
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APPLICATION NUMBER: 60/074330 FILING DATE: 22-JAN-1998 PRIOR APPLICATION DATA:

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RESULT 4
US-09-234-340A-71
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; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-71
                                                            Sequence 71, Application US/09234340A

Patent No. 6468532

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Genentech, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Dresta, Leonard G.
APPLICANT: Drasta, Gerardo A.
APPLICANT: Zapata, Gerardo A.
APPLICANT: Zapata, Gerardo A.
APPLICANT: OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
ITITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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Best Local S
Matches 411
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FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICCHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-5530
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
       COUNTRY:
                    CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
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RESULT 5
US-08-157-101A-7
; Sequence 7, Application
; Patent No. 5808032
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US/08157101A

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PRIOR APPLICATION:

APPLICATION NUMBER: US/09/121,952

APPLICATION NUMBER: US/09/121,952

FILING DATE: 24-Uul-1998

APPLICATION NUMBER: 60/074330

FILING DATE: 22-JAN-1998

PRIOR APPLICATION NUMBER: 60/075467

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: LOVE, Richard B.

REGISTRATION NUMBER: 34,659

REGISTRATION NUMBER: 91085R4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEPAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids

TYPE: Amino Acid

TYPE: Amino Acid

TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/234,340A FILING DATE:
                                                                                        361
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                        RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                     EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                              DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                           YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                               GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                       GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                SSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPELL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                       SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
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Best Local Simi
Matches 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURIOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEPAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 NEW CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                      GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNSKNTLYLEVKSLQTEDTGVYYCIRDQTYGVHRFDSWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                    SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-LGTYYFDSWGQGTLLTVSS 119
                  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                              PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                GLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                             ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLVESGGGVVQPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVILYDGNHKFY
                                                                                                                                         PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.5%; Score 2194.5; DB 1; Length 459;
91.8%; Pred. No. 2.3e-161;
ative 15; Mismatches 21; Indels 1;
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US-08-466-151-8
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Best Local Similarity
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APPLICANT: Jardieu,
APPLICANT: Presta, 1
                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/08/466,151
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/744
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SUNDAGE CTAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/405
PILING DATE: 15-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879
FILING DATE: 07.MAY-1002
                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/44
FILING DATE: 06-Jun-1995
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                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                  LENGTH: 453 amino
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Svoboda, Craig G
REGISTRATION NUMBER: 39
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ZIP: 94080
                                                                                                                                                                                                                                                                                 TOPOLOGY:
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118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFFAV
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                                                      YADSVKGRFTISRDDSKNTFYLQMNSLRABDTAVYYCARGSHYFGHWHFAVWGQGTLVTV
                                                                            YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV
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                                                                                                                    EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN
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                                                                                                                                                                                                                                                                                   Linear
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                                                                                                                                                                                            70.6%; Score 2169; DB 3; 91.0%; Pred. No. 2.1e-159; ative 16; Mismatches 19;
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65
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                                                                                                                                                                                                                             Length 453;
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE DE INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR PPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-05-07
PRIOR FILING DATE: 1991-08-14
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US-08-466-163B-8
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Best Local S
Matches 413
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LENGTH: 453
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence FEATURE:
                       236
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LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRE
                                                                                                                                 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
                                                                                                                                                      SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
                                                                                                                                                                                                    YADSVKGRFTISRDDSKNIFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV
                                                                                                                                                                                                                                         YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV
                                                                                                                                                                                                                                                                                                       EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY
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                                                       LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE
                                                                           LQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE
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; Pred. No. 2.1e-159;
16; Mismatches 19;
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: PCT/US92/0660
PRIOR APPLICATION NUMBER: PCT/US92/0660
PRIOR FILING DATE: 1992-08-14
PRIOR PILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PRILING DATE: 1991-08-14
PRIOR PRILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
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SEQ ID NO 8
LENGTH: 453
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: humanized maell, version 1 heavy chain
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Best Local Similarity
Matches 413; Conserv
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RESULT 9
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR PPLICATION NUMBER: US 07/85,899
PRIOR PPLICATION NUMBER: 05-08-06-06
PRIOR PILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PILING DATE: 1991-08-14
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Best Local S
Matches 413
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Patent No. 6699472
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SEQ ID NO 8
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OTHER INFORMATION: humanized maell, version 1 heavy chain
-09-802-077-8
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as
FILE REFERENCE: P0718P2C2US
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TYPE: PRT
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TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula
TITLE OF INVENTION: Improved Anti-IgE Antibodies and
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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MEDIUM TYPE: 3.5 inch, 1.44 Mb flc

MEDIUM TYPE: 3.5 inch, 1.44 Mb flc

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WINPATIN (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,352E

FILING DATE: 03-Jul-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: SYODOGA, Craig G.

REGERENCE/DOCKET NUMBER: 91123

TELEPHONE: 650/225-1489

TELEPHONE: 650/225-1489
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TOPOLOGY: I.in-
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                DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                               GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                        YSDSVKGRFTISRDNSKNTLYLOMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV
 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                               YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                              GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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90.9%; Pred. No. 3e
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Method of
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RESULT 11 US-08-887-352B-16

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Sequence 16, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leona
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FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 91,04
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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STREET: 1 L...
CITY: South San Fra
CTATE: California
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TITLE OF INVENTION:
TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acid
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                                               YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
                                                                                                                              GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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outh San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
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US-08-466-151-65
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/879495
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
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                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
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1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe FILE REFERENCE: Improved Anti-IgE Antibodies and Method of Improving Polype; CURRENT APPLICATION NUMBER: US/09/109,207C; CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14
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US-09-109-207C-14
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Matches 411
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
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                                                        SSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL SGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
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                 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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                                                                                                                                                                                                                                                                                                Score 2167; DB 3;
Pred. No. 3e-159;
5; Mismatches 21;
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PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
LENGTH: 451
TYPE: PRT
RGANISM: Artificial
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US-09-109-207C-16
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US-09-109-207C-16
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Prei
TITLE OF INVENTION: Improved Anti-IgE Anti!

FILE REFERENCE: P1123R1

FULE REFERENCE: P123R1

FULE REFERENCE: P1123R1

FULL REFERENCE: P1123R1

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NAME/KEY: Artificial
LOCATION: 1-451
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RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Improved Anti-IgE Antibodies and Method of Improving Polypeptide
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GENERAL INCOMPATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
ITITE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT PILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1999-07-07
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOME SEQ I
Search completed: December 23, 2004, 19:07:50 Job time: 40.4376 secs
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US-09-296-005-14
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Perfect score:
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1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

15: /cgn2 6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

18: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

19: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

10: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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  US-10-138-727A-41
US-10-310-719-32
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US-10-310-719-37
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US-10-320-231A-79
US-10-704-522-6
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Sequence 41, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 37, Appl
Sequence 35, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 32, Appl
Sequence 33, Appl
Sequence 79, Appl
Sequence 79, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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## ALIGNMENTS

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PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 579
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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Publication No. US20030157054A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Susan
TITLE OF INVENTION: Recombinant Tumor Specific And
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/10/138,727A
CURRENT APPLICATION NUMBER: US/10/138,727A
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                                                                                                                                                                                  Query Match 89.6%; Score 2750.5; Best Local Similarity 88.5%; Pred. No. 8.2c Matches 516; Conservative 32; Mismatches
61 ADDFKGRFAFSLETSTSTAFLQINNLRSEDTATYFCVRFISKGDY----WGQGTSVTVSS
                                       61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYYFDSWGQGTLLTVSS 119
                                                                                            1 QIQLVQSGAEVKKPGETVKISCKASGYTFTNYGMNMVKQTPGKGLKMMGWINTYTGEPTY
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CURRENT APPLICATION NUMBER: US/10/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR FILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 579
TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-310-719-32
Sequence 32, Application US/10310719
Publication No. US20030166163A1
GENERAL INFORMATION:
GENERAL INFORMATION: Stephen
TITLE OF INVENTION: Immunocytokines With Modulated
FILE REFERENCE: LEX-020
                                                                                                                                                                                                                                                                                                                      Query Match 89.6
Best Local Similarity 88.5
Matches 516; Conservative
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OTHER INFORMATION: dI-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant-10-310-719-32
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                           ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                   89.6%; Score 2750.5; DB 1.
88.5%; Pred. No. 8.2e-166;
ative 32; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: LEX-023
CURRENT APPLICATION NUMBER: US/10/737,208A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: US 60/433,945
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
FILING ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 518; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10737208A Publication No. US20040203100A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gillies, Stephen D.
APPLICANT: Lo, Kin-Ming
TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 575
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                                                                                                                                                                       STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFFAVLQSSG
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                                                  LYSISSVVTVPSSSIGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELIGGP
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es 33;
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Sequence 37, Application US/10310719

Publication No. US20030166163A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
ITITLE OF INVENTION: Immunocytokines With Modulated Selectivity
FILE REFERENCE: LEX-020
CURRENT APPLICATION NUMBER: 00/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR APPLICATION NUMBER: 60/371,966
PRIOR PILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/371,966
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 580
TYPE: PRT
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US-10-310-719-37
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; OTHER INFORMATION: dI-NHS76(gamma4h)(FN>AQ)-ala-IL2(D20T)
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37
                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.3%;
Best Local Similarity 85.8%;
Matches 500; Conservative 29
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                  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQAQ 297
                                       PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                           GLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                              ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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; Pred. No. 1.3e-157;
29; Mismatches 50;
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US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated
; FILE REFERENCE: LEX-020
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US-10-310-719-35
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PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 580
TYPE: PRT
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Best Local (
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CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR FILING DATE: 2001-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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297
                299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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QSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSRE
                                                                     GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQA
                                                                                            GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                           SGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVEPKSCDKTHTCPPCPAPP-VA
                                                                                                                                                              SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                  GASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                        YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGKWSK--FDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                          YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                   84.3%; Score 2589; DB 14;
85.1%; Pred. No. 1.4e-155;
tive 29; Mismatches 52;
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APPLICANT: BIGGEN, INC.
APPLICANT: BIGGEN, INC.
FILE REFERENCE: A101 PCT
CURRENT APPLICATION UMBER: US/10/474,832
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/283,794
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 70
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 447
TYPE: PRT
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US-10-474-832-4
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Best Local Similarity
Matches 426; Conserv
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                 361
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TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                          TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
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                                                                                                                   SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                                                       LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
                                                                                                                                                                       LYSLSSVYTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
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                                          TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
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Pred. No. 4.8e-134;
4; Mismatches 17; I
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GENERAL INFORMATION:
APPLICANT: BICCEN, INC.
TITLE OF INVENTION: ANTIBODIES TO VLA-1
FILE REFERENCE: A101 PCT
CURRENT FILING DATE: 2003-10-14
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/283,794
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: polypeptide
US-10-474-832-5
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US-10-474-832-5
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LENGTH: 447
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Best Local Similarity 94.9%;
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             QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
                                                                       TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
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                                                                                                                                TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
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QGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                        TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
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Pred. No. 1.1e-133;
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RESULT 9 US-10-412-406-32 ; Sequence 32, Application US/10412406 ; Publication No. US20040058394A1

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RESULT 9
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
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APPLICANT: SALDHANA, JOSE W.
APPLICANT: SALDHANA, JOSE W.
FIITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINA10CN
CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT APPLICATION NUMBER: 60/240,285
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR APPLICATION NUMBER: PCTUSO1/32140
PRIOR APPLICATION NUMBER: PCTUSO1/32140
PRIOR APPLICATION NUMBER: PCTUSO1/32140
PRIOR APPLICATION NUMBER: PCTUSO1/32140
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Best Local Similarity
Matches 422; Conserv
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APPLICANT: BIOGEN, INC.
APPLICANT: GARBER, Ellen
APPLICANT: LYNE, Paul
APPLICANT: SALDHANA, Jose W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINA100CN
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SOFTWARE: FastSEQ for Windows Version
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APPLICANT: GARBER
APPLICANT: LYNE,
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TYPE: PRT
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 33
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Best Local Similarity
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ORGANISM: Homo
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Sequence 6, Application US/10474832
Publication No. US20040081651A1
GENERAL INFORMATION:
APPLICANY: BIOGEN, INC.
TITLE OF INVENTION: ANTIBODIES TO VLA-1
FILE REFERENCE: A101 PCT
CURRENT APPLICATION NUMBER: US/10/474,832
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/283,794
PRIOR APPLICATION NUMBER: 60/283,794
PRIOR APPLICATION NUMBER: 60/303,689
PRIOR APPLICATION NUMBER: 60/303,689
PRIOR PILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: PCT/US01/32140
PRIOR APPLICATION NUMBER: PCT/US01/32140
PRIOR FILING DATE: 2001-10-12
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Pred. No. 2.5e
8; Mismatches
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; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE: OTHER INFORMATION: Description; OTHER INFORMATION: polypeptide US-10-474-832-6
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US-10-320-231A-79
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                                                                                                                    APPLICANT: Neben, Steven
APPLICANT: Neben, Steven
APPLICANT: Takeuchi, Toshihiko
APPLICANT: Takeuchi, Toshihiko
APPLICANT: Tokkinson, Adrian
TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use |
TITLE OF INVENTION: Treatment Of Asthma
FILE REFERENCE: 7430*163
CURRENT APPLICATION NUMBER: US/10/320,231A
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/342,174
PRIOR PILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn version 3.2
SEQ ID NO 79
LENGTH: 445
TYPE: DBT
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Best Local S
Matches 424
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          Query Match
Best Local Similarity
Matches 421; Conserv
                                                            FEATURE:
OTHER INFORMATION:
-10-320-231A-79
                                                                                                ORGANISM: Artificial
                                                                                                             TYPE: PRT
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              Conservative
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                                                                        synthetic sequence
                     72.8%;
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           Score 2234.5; DB 14;
Pred. No. 2.7e-133;
7; Mismatches 17; I
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Pred. No. 2.1e-133;
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Sequence 6, Application US/10150475A

Publication No. US20030103985A1

Publication No. US20030103985A1

APPLICANT: AGOLf, G. et al.

APPLICANT: AGOLf, G. et al.

FILE REFERENCE: 1/1211

CURRENT APPLICATION NUMBER: US/10/150,475A

CURRENT FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: US 60/307,451

PRIOR FILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1
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US-10-150-475A-6
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LENGTH: 444
TYPE: PRT
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Humanised
OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    Local Similarity
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APPLICANT: Adolf, Gunther
APPLICANT: Baumann, Michael
APPLICANT: Heider, Karl-Heinz
APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and methods for treating cancer using
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REFERENCE: 1/1414
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: US/10/704,522
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: US 60/429,516
PRIOR APPLICATION NUMBER: EP 02024881
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 6
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US-10-704-522-6
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Best Local Similarity
Matches 421; Conserv
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TYPE: PRT
ORGANISM: Artificial Sequence
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TYRVVSVLTVLHQDWLNGKEYKCKVSNKAL.PAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                    SVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
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Publication No. US20040126379A1

GENERAL INFORMATION:

APPLICANT: Hedolf, Guenther

APPLICANT: Heider, Karl-Heinz

TITLE OF INVENTION: Compositions and Methods for Treating Cancer using

TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and

TITLE OF INVENTION: Chemotherapeutic Agents

FILE REFERENCE: 1/1383

CURRENT APPLICATION NUMBER: US/10/645,215

CURRENT FILING DATE: 2003-08-21

PRIOR APPLICATION NUMBER: EP 02 018 686.2

PRIOR APPLICATION NUMBER: US 60/405,956

PRIOR FILING DATE: August 21, 2002

PRIOR FILING DATE: August 26, 2002

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1

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US-10-645-215-6
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TYPE: PRT
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QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444

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CURRENT APPLICATION NUMBER: US/09/736,371B
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 9815909.8
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: PCT/GB99/02380
PRIOR APPLICATION NUMBER: PCT/GB99/02380
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 449
TYDE: PRT
ORGANISM: Homo sapiens
US-09-736-371B-21
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US-09-736-371B-21

; Sequence 21, Application US/09736371B

; Patent No. US20020131968A1

; GENERAL INFORMATION:
Search completed: December 23, 2004, 19:35:46 Job time : 134.396 secs
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APPLICANT: Erewin, Mark
TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
FILE REFERENCE: Waldmann
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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A, Molecule type: pa A, Rolecule type: pa A, Residues: 136-154 A, Note: this sequen R, Ponstingl, H.; Hi Hoppe-Seyler's Z. P A, Title: Die Primae	A; Molecule A; Residues A; Residues R; Rutishaus Biochemistr A; Title: Th A; Teference A; Conseion	A; Molecule type: DNA A; Residues: 88-113; 2 A; Cross-references: R; Cunningham, B.A.; Biochemistry 9, 3161 A; Title: The covalen A; Reference number: A; Contents: myeloma A; Accession: B90563	A;Accession: S36861 A;Molecule type: DNA A;Residues: 2-330 <har: 1982="" 29,="" 671-679,="" a;accession:="" a;cross-references:="" a;reference="" a;title:="" cell="" em="" j="" n.;="" number:="" of="" r;takahashi,="" s31887="" s33887<="" structure="" td="" ueda,=""><td>A; ROLECULE LYPE: DNA A; Residues: 1-330 &lt; E A; Cross-references: 1 A; Note: this sequence A; Note: Lys-330 is r R; Harris, L.J. A; Reference number: 1</td><td>RESULT 1  GHHU  GHHU  C;Species: Homo sap  C;Date: 31-Jan-1981  C;Accession: A93433  R;Ellison, J.W.; Be  Nucleic Acids Res.  A;Title: The nucleo  A;Reference number:  A;Accession: A93433  A.Molecule type.</td><td></td><td>00004444 00000000000000000000000000000</td></har:>	A; ROLECULE LYPE: DNA A; Residues: 1-330 < E A; Cross-references: 1 A; Note: this sequence A; Note: Lys-330 is r R; Harris, L.J. A; Reference number: 1	RESULT 1  GHHU  GHHU  C;Species: Homo sap  C;Date: 31-Jan-1981  C;Accession: A93433  R;Ellison, J.W.; Be  Nucleic Acids Res.  A;Title: The nucleo  A;Reference number:  A;Accession: A93433  A.Molecule type.		00004444 00000000000000000000000000000
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pe: protein 36-154,'Q',156-165,' 8equence has the Glm H.; Hilschmann, N. E. Z. Physiol. Chem. Primaerstruktur eine	A; Molecule type: protein A; Residues: 1-96; 'R', 98-135 <cun> A; Residues: 1-96; 'R', 98-135 <cun> A; Rote: this sequence has the Glm(3) R; Rutishauser, U.; Cunningham, B.A.; Biochemistry 9, 3171-3181, 1970 A; Title: The covalent structure of a A; Reference number: A90564; MUID:710 A; Contents: Eu A; Contents: Eu A; Contents: Eu A; Contents: Eu</cun></cun>		\$36861 YPG: DNA 2-330 <har> 2-330 <har> rences: EMB N.; Ueda, -679, 1982 -cture of h number: \$33 \$33887</har></har>	A; MOLECULE CYPE: DNA A; RESIDUES: 1-330 ASILI> A; Cross-references: UNIPROJ A; Note: this sequence has t A; Note: Lys-330 is removed R; Harris, L.J. R; Harrisded to the EMBL Data A; Reference number: 833904	n C regi sapiens 1981 #se 1981 #se 3433; S3 433; S3 ces: 10, ces: 10, cleotide cleotide 3433		222222235 4566674845 4566677272
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.65,'Q',167-176,'Q',178-194,'N',196-197 .Glm(non-1) markers, 239-Glu and 241-M N. .em. 357, 1571-1604, 1976 .eines monoklonalen IgG1-Immunglobulins	A; Molecule type: protein A; Molecule type: protein A; Residues: 1-96,'R', 98-135 <cun> A; Residues: 1-96,'R', 98-135 <cun> A; Note: this sequence has the Glm(3) marker, 97-Arg R; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H Biochemistry 9, 3171-3181, 1970 Biochemistry 9, 3171-3181, 1970 A; Title: The covalent structure of a human gammaG-immunoglobulin. A; Reference number: A90564; MUID:71064025; PMID:5530842 A; Contents: Eu. 200564</cun></cun>	TAK> 1370 13er, U.; Gall, W.E.; Gottlieb, P.D.; 1 1970 1970 MUID:71064024; PMID:5489771 Eu	NA NA KHAR>  EMBL:Z17370  eda, S.; Obata, M.; Nikaido, T.; Nakai, in the control of human immunoglobulin gamma genes: im cf human immunoglobulin gamma genes: immunogl	EMBL:217370 7) allotypic marker, anglation October 1992	RESULT 1  GHHU  GHHU  GY gamma-1 chain C region - human  C;Species: Homo sapiens (man)  C;Species: Homo sapiens (man)  C;Accession: A93433;  R;Ellison, J.W.; Berson, B.J.; Hood, L.E.  R;Ellison, J.W.; Berson, B.J.; Hood, L.E.  R;Ellison A9483;  R;Reference number: A93433; MUID:82274238; PMID:6287432  A;Accession: A93433  A,Malecule Arms. NAM  A;Malecule Arms. NAM  A;Malec	ALIGNMENTS	G2MSBM I47162 S04845 S69131 B46529 B46529 A36040 A49444 S38950
A;Molecule type: protein A;Molecule type: protein A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240, A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240, A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met A;Ponstingl, H.; Hilschmann, N. R;Ponstingl, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A;Title: Die Primaerstruktur eines monokionalen IgG1-Immunglobulins (Myelomprotein Nie),	rg, w.H.; Edelman, G.M. obulin. VIII. Amino acid sequ	P.D.; Waxdal, M.J.; Edelman, obulin. VII. Amino acid seque	, S.; Honjo, T. implications for evolution of a	97-Lys, and the Glm(1) markers,	hange 09-Jul-2004 8; A91723; A02146 C-gammal gene.		Ig gamma 2b chain Ig gamma 4 chain c Ig gamma 4 chain c Ig heavy chain WHI Ig heavy chain (DO Ig Y heavy chain (CO Ig Y heavy chain V-I Ig heavy chain V-I Ig gamma-1 heavy c Ig gamma-1 heavy c

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A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid A;Reference number: A90565, MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
[20-85/Domain: immunoglobulin C region; immunoglobulin homology
[313-206/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;109,112/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
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A;Reference number: A91668; MUID:77070269; PMID:826475

A;Contents: myeloma protein Nie

A;Accession: B91668

A;Molecule type: protein

A;Residues: 1-34, 'Q',36-96, 'K',98-115, 'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27

A;Note: this sequence has the Gim(17) and Gim(1) markers

R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL

A;Reference number: A91723; MUID:83289131; PMID:6884994

A;Contents: myeloma protein KOL; disulfide bonds

A;Accession: A91723

A;Accession: A91723

A;Molecule type: protein

A;Residues: 1-96, 'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH

A;Note: this sequence has the Gim(3) and Gim(non-1) markers

B;Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

h.Title. The corelant errorers of a human cammaG-immunoclobulin X. Intrachain disulfid
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                         QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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A23511

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - hums C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.1
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma A;Reference number: A23511; MUID:86148507; PMID:31
A;Accession: A23511
A;Accession: A23511
A;Rolecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g331
C;Genetics:
A,Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A,Reference number: A60764; MUID:90007613; PMID:2571587 A,Accession: A60764
A,Status: preliminary A,Molecule type: DNA A,Residues: 1-377 <HUC> A,Residues: 1-377 <HUC> A,Cross-references: UNIPROT:Q8N4Y9 C,Superfamily: immunoglobulin C region; immunoglobulin bC,Keywords: immunoglobulin
                                                                                                                                                                                     Ig gamma-3 chain C region, form LAT - h
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision
C;Accession: A60764
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A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
A;Superfamily: immunoglobulin
C;Keywords: immunoglobulin
C;Keywords: immunoglobulin
bomology <IMM>
                                                                                                                                                          R;Huck, S.; Lefranc, G.; Lefranc, Immunogenetics 30, 250-257, 1989
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Pred. No. 3e-
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C;Species: Homo sapitens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-
C;Accession: A33906; A92809; A90752; A93132; A02148
R;Ellison, J; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;7itle: Linkage and sequence homology of two human immunoglobulin gamm
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:PO1859; GB:V00554; GB:J00230; NID:g32759; P
A;Cross-references: UNIPROT:PO1859; GB:V0
                                                                         A,Title: The amino acid sequences of the three heavy chain A;Reference number: A90752; MUID:80001357; PMID:113060 A;Contents: myeloma protein Zie A;Accession: A90752 A;Molecule type: protein A;Residues: 1-24,'E', 26-57,'EV', 60-85;132-171,'ZZZ',175,'B'A;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
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;Title: A note on the amino;Reference number: A93132; N;Contents: Zie
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                            The amino acid sequence of residues 381-391 A93132; MUID:80114419; PMID:118920
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Pred. No. 3.9e-84
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                                                      human
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                                                      immunoglobulin
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RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence revision 02
C;Accession: A90933; A90249; A02150
C;Accession, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human i
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A;Cross-references: GDB:119338; OMIM:147110

A;Map position: 14932.33-14932.33

C;Complex: An immunoglobulin feterotetramer subunit consists of two identical light (ka; hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM3>
F;139-306/Domain: immunoglobulin homology <IM3>
F;147Dsulfide bonds: interchain (to light chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human: A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Reference annotation; myeloma protein Sa, disulfide box R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Mature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March
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A; Contents:
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                         QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                          LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                               STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE
                                                                                                                                                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                            PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN
                                                                                                                                                                                                                                                                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                              MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW
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ilarity 91.2%;
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Pred. No. 7.7e-83;
2; Mismatches 13;
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sequence of a human

immunoglobulin

C-gamma4

02-Apr-1982

#text\_change

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A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Accession: A90933
A;Accession: A90933
A;Accession: A90933
A;Accession: A90933
A;Residues: 1-327 <ELL>
A;Cross-references: UNIFROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Parrial amino acid sequence of the constant
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Genetics: A;Gene: GDB:119340; OMIM:147130
A;Residues: 1-30;81-326 <PIN>
C;Genetics: A;Gene: GDB:119340; OMIM:147130
A;Map position: 14932.33-14932.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (A)
C;Superfamily: immunoglobulin c region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-48/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;144-203/Domain: immunoglobulin homology <IM1>
F;27-83,141-201,247-305/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: interchain (to heavy chain) #status experimental
F;105,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted
monocional antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.;
Blochem. Blophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibod
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Molecule type: protein
A;Residues: 1-444 <AXA>
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Pred. No. 4.4e-82;
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SNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK
                                                                                                            QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                     ---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWEVDDVEVHTAQTQPREE
                                                                                                                                                                                  LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                              D-LYTLSSSTWPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV
                                                                                                                                                                                                                                                                                                  SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
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                SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                     KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQK
                                                                      RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                        SGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPEL
                                                                                                                                                                                                                                                                                     SAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                             KYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCRTP-WVYAMDCWGQGTSVIVS
                                                                                                                                                                                                                                                                                                                                                                        YYSDSVKGRFTISRDNSKNTLYLOMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVS
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Pred. No. 2.5e
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                            449
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A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PIDR;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bowine immunoglobulin constant region hea A;Reference number: \$06610; MUID:90097956; PMID:2513487
A;Reference number: \$06610; MUID:90097956; PMID:2513487
A;Residues: 142-470 <SYM>
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membr F;161-225/Domain: immunoglobulin homology <IMM> R;Sanders, P.G.
submitted to the EMBL D
A;Reference number: S22
A;Accession: S22080
A;Status: preliminary Ig heavy chain precursor (B/MT.4A.17.H5.A5) - Walternate names: Ig gamma-1 chain C region C; Species: Bos primigenius taurus (cattle) C;Date: 06-Jan-1995 #sequence revision 06-Jan-C;Accession: S22080; S06610; A31303 A; Molecule type: mRNA A; Residues: 1-470 <SAN> BL Data S22080 Library, November 1991 06-Jan-1995 (clone 8.10) #text\_change heavy PID: 9440 chain gamma

> and

gamm

immunoglobulin homology
r; immunoglobulin; membr

membrane

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257

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A;Status: preliminary
A;Molecule type: mkNA
A;Residuss: 1-469 < LOUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1;
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
E;276-345/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
$37483

I gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accession: $37483
R;Ducancel, F.F.D.
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Best Local S
Matches 267
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Best Local :
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                                                                                                                                                                                                                 16.9%; 18; 18; 267; Conservative 7
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                                                                                                                                                                 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKPREE
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AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTPPAVLQSD 199
                   ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS 179
                                                                        NENFKGKATLTVDTSSSTAYMOLSSLTSEDTAVYFCARAMGATATLLDYWGQGTTLTVSS
                                                                                           SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT-YYFDSWGQGTLLTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY----YFDSWGQGTLLT 116
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                                                                                                                                                                                                                 Score 1440.5; DB
Pred. No. 1.7e-73;
12; Mismatches 108
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Pred. No. 4.3e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           February 1993
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                                                                                                                                                                                                                                                     DB 2;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Koywords: disulfide bond; glycoprotesin; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-244/Domain: C region <CHR>
F;118-214/Domain: C region <CH2>
F;215-230/Region: hinge
F;215-230/Region: hinge
F;211-340/Domain: C2 region <CH2>
F;211-446/Domain: C3 region <CH3>
F;311-446/Domain: immunoglobulin homology <IMM>
F;114-46/Domain: immunoglobulin homology <IMM>
F;117/Domain: C3 region <CH3>
F;117/Domain: G3 region <CH3>
F;118-446/Domain: immunoglobulin homology <IMM>
F;118-446/Domain: immunoglobulin homology <IMM>
F;118-446/Domain: interchain (bonds: #status predicted
F;123/Disulfide bonds: interchain (to light chain) #status predicted
F;123/Disulfide bonds: interchain #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
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C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Welsgerber, C., C., submitted to the EMBL Data Library, January 1993
A. Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against A.Reference number: S40295
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A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision
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 178
                                181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP---CPAPELLG
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                                                                                                                                       QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY
                                                                                                                                                                                                                                      EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLG
                                                                                                                                                              SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEMTKKQVTLTCMVTDFMPED1YVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE 377
                                                                        KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD-
                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                         46.8%; Score 1437; DB 2; 59.3%; Pred. No. 2.5e-73; tive 70; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-Apr-1994 #text_change 09-Jul-2004
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4

177 180

236 238 120

60 60

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RESULT 10

S31459

Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domest C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_c C;Accession: S31459
R;Patri, S:, Mau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Accession: S31459
A;Accession: Breliminary
A;Molecule type: mRNA
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 cPAT-
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin hom C;Reywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                               CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                               DIDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWG
                YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                       YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFL
                                                                                                                                TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                          QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWL-----GGSGYDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
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                                                                                                               TKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQV
                                                                                                                                                                         CPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTAR
                                                                                                                                                                                                                                                                                          PGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                    QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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                                                       YVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADGSYFL
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                                                       431
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RESULT

11

Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Als musculus (house mouse)
C;Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzall submitted to the EMBL Data Library, July 1992
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neota; A;Accession: S25057
A;Accession: S25057
A;Status: preliminary

Kreuzaler,

neotop specific

RESULT 12 G2MS11

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Ig heavy chain V region precursor - human
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 19-Mar-1997 ##equence_revision 19-Mar-1997 #text_change 01-Dec-2000
(;Accession: $69339; $72664
R;Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition A;Reference number: $69339; MUID:95262687; PMID:7744049
A;Recession: $69339
A;Status: preliminary
A;Accession: $69339
A;Status: preliminary
A;Residues: 1-374 <KHA
A;Resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S72664
A;Accession: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Best Local Sin
Matches 282;
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Local Similarity 62.1%;
les 282; Conservative 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QITLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVGVGWIRQPPGQALEWLALI-FWDDDK 78
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                      KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                    SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                                                                                                                           SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                                                                                                                                                                                                                         EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
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Pred. No. 5.7e-73;
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A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>C;Comment: The a allele sequence is shown.
C;Comment: The a allele sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light C;Complex: An immunoglobulin haterotetramer subunit describes into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog F;157-222/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;0llo, R.; Rougeon, F.
R;0llo, R.; Rougeon, F.
Nature 296, 761-763, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Structure of the constant and 3' untranslated regions A,Reference number: A26235; MUID:80081501; PMID:117548 A,Contents: MPC 11
A,Accession: A26225
A;Molecule type: mRNA
A,Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TUI>A;Note: Lys-474 is probably removed posttranslationally R,Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner Science 206, 1303-1306, 1979
                                                                                                                                                                                                                                                     F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
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R;Kim,
J. Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence of the cloned gene for the constant region A;Reference number: A26232; MUID:80081502; PMID:117549 A;Accession: A26232 A;Molecule type: DNA A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TUZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: the sequence was determined from the R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Science 206, 1299-1303, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Crose-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
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A;Reference number: A26233; MUID:82173203;
A;Contents: b allele
A;Accession: A26233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 138-161,'L', 163-189,'FP',193-474 < YAM>
A; Cross-references: GB: J00461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete nucleotide sequence of immunoglobulin A;Reference number: A02157; MUID:80120716; PMID:6766534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: a allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA; Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474; Cross-references: GB: J00461
                                                                                                                                                                          Matches
                                                                                                                                                                        260;
80
                                      13
                                                                                      20
                                                                                                                                                                                                 Similarity
                                      SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY---YFDSWGQGTLLTV 117
                                                                                    EVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDGTKF
                                                                                                                             EVOLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY
                                                                                                                                                                                            45.3%;
                                                                                                                                                                          72;
                                                                                                                                                                   Score 1390; DB 1;
Pred. No. 1.2e-70;
2; Mismatches 113;
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3; PMID:6803173
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Best Local Similarity
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411
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KLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 449
                                                                                           YILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYS
                                                                                                                       YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPFVLDSDGSFFLYS
                                                                                                                                                                                                                                  TKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                      CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
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                                                                                                                                                                                              TOTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQV
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F;1-19/Domain: signal sequence #status predicted <SIG>F;20-475/Product: Ig gamma-2b chain #status predicted F;159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                       A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                           Ride Waele, P.; Feys, V.; van de Voorde, A.; Molemans, I
Eur. J. Biochem. 176, 287-255, 1988
A;Title: Expression in non-lymphoid cells of mouse recor
A;Reference number: S01320; MUID:88329081; PMID:3138116
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision
                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-475 < DE1>
                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession:
R;de Waele,
                                                                                                    C; Keywords: immunoglobulin
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ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS NEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQVGLLPFGYWGQGTLVTASA SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-LGTYYFDSWGQGTLLTVSS

179

139

119

79

PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDXKLEPSGPTSTINPCPPCKECHKCP GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP-----CP AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S

292

258 232 198

APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQ

80 61 20 257;

Conservative

44.5%;

Score 1367.5; DB Pred. No. 2.1e-69; 5; Mismatches 116

116;

9

2

Length

QVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGNSYF EVOLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY

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Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_chan;
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_cha
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interacti
A;Reference number: S31866
A;Accession: S31866
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A;Accession: S31866
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S31866
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Matches 231; Conserv
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                                                                                                                                                                                                                                                                        RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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; Pred. No. 9.4e
43; Mismatches
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A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:G;Keywords: immunoglobulin
F;1-22/Region: Bscherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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Best Local Similarity
Matches 233; Conserv
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PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
                                                                                                                                 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                  EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                          TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                           TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                        PAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPE
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                    EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
                                                                                                                                                                                                                                                41.0%;
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                                                                                                                                                                                                                                 Score 1260; DB of Pred. No. 1e-63; O; Mismatches
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Search completed: December 23, 2004, 19:06:04 Job time: 33.449 secs

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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
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3071
1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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CAE45781
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Q7Z5W1
Q6F055
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CAE45920
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Cae45920 homo sapien Bac85232 homo sapien Q6in78 homo sapien Q6in78 homo sapien Q6in78 homo sapien Q6in78 homo sapien Aah06402 homo sapien Aah19046 homo sapien Bac8544 homo sapien Bac85774 homo sapien Cae45774 homo sapien Cae45774 homo sapien Cae45774 homo sapien Aah65820 homo sapien Bac85388 homo sapien Bac85388 homo sapien Bac85388 homo sapien Aah64466 homo sapien Bac85388 homo sapien Bac85381 homo sapien Bac85381 homo sapien Bac85385 homo sapien Bac85381 homo sapien
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Cae45972 homo sapi
                                                                                                                                                                                                                                       Q6pi81 homo sapien
Aah41037 homo sapi
                                                                                                                                                                                                                                                        Q6pja4 homo sapien
Aah18747 homo sapi
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SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR--VKLGTY-YFDSWGQGTLLTV 117

6 68 3 441 2 CAB45773 Bac85171 Bac85171 bmmo 6 67.8 467 2 BAC85171 Bac85171 bmmo 5 67.8 472 2 BAC85171 Bac85171 bmmo 5 67.8 470 2 BAC85236 ABAC8236 ABAC8236 bmmo 6 67.8 470 2 BAC85236 BAC85017 BAC85171 bmmo 6 67.6 476 2 BAC8517 BAC8517 BAC85171 bmmo 6 67.6 478 2 BAC8517 BAC8517 BAC8517 BAC8517 bmmo 6 67.6 478 2 BAC8517 BAC8517 BAC8517 bmmo 6 67.4 473 2 BACC8517 BAC8517 BAC8517 bmmo 6 67.4 473 2 BAC8517 BAC8517 BAC8517 BAC8517 bmmo 6 67.4 473 2 BACC8513 BAC8517 BAC8517 bmmo 6 67.4 473 2 BACC8517 BAC8517 BAC8517 BAC8517 bmmo 6 67.4 473 2 BACC8517 BAC8517 BAC8517 BAC8517 bmmo 6 67.4 473 2 BACC8517 BAC8517 BAC8	망	Query I Best L Matche		RA BOBAK RA Richa RA Villa RA Fahey RA Blake RA ROdri RA Krzyw RA Jones RT "Genee RT "Genee RT and m RT Proc. RN [2]		H2	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
ELIMINARY; PRT; 471 AA.  PRELIMINARY; PRT; 471 AA.  PEMBLrel. 27, Created)  AAR 28 BACO5012  ALIGNMENTS  ALIGNMENT		2 1 1 1		ak S.A., lands S.A., lalon D.K. lalon D.K. ey J., He ting M., l keeley R.I ke	ENCE H UE=Spl INE=22 usberg sner H chul S ins R. chenko chenko	ILT 1  AAH24289  AAH24289; 02-MAR-2004 02-MAR-2004 02-MAR-2004 Hypothetical Homo sapiens Eukaryota; M Mammalia; Eu	60075 60075 60075 60075 60075 60075
EAC65171 BAC65173 BAC65171 BAC65225 BAC6525 BAC6525 BAC6525 BAC6525 BAC6525 BAC6525 AAA62336 BAC05017 BAC05017 BAC05012 BAC05012 BAC05013 BAC05012 BAC05013			N.A. ; 3-2002) 3-AAH24 protein. L AA; 5	Ewan P. Forley K Muzny Muzny (dan A., Touch , Grimw , Grimw , Skal irra M. A d initi , sequen ad. Sci	M N.A. n; A., Fein L., Fein Collin Collin Marusi Marusi Soares Soares	RELIMIN TrembLi TrembLi TrembLi (TrembLi (Humneir (Humnai) tazoa; heria;	* * * • • • • • • • • • • • • • • • • •
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Cae45773 homo Bac86225 homo Bac86225 homo Bac86225 homo O7z7p5 homo si Aah62336 homo Bac05013 homo Bac05012 homo Bac05012 homo Bac05013 homo Bac05013 homo Bac05013 homo Bac05013 homo Bac05014 homo Bac05013 homo Bac05014 homo Bac05015 homo Bac05016 homo Bac05017 homo Bac05018 homo Bac05018 homo Bac05018 homo Bac05019 homo Bac05019 homo Bac05011 homo Bac05011 homo Bac05011 homo Bac05011 homo Bac05012 homo Bac05013 homo Bac05013 homo Bac05013 homo Bac05013 homo Bac05013 homo Bac05011 homo		<pre>core 2226.5; DB 2; red. No. 7.7e-137;    Mismatches 14; CAASGFAFSHYAMSWVROAF</pre>	MBL/GenBank/DDBJ dat 388F7F4CF588660E (	man K.J., Malek J S., Garcia A.M., Cergren E.J., Lu X. M., Madan A., Rodr. C., Shevchenko Y., Green E.D., Dicke chmutz J., Myers R mailus D.E., Schnes is of more than 15		ated) t sequence update) t annotation update t annotation taniata; Vertebrata	AAH12937  BAC85175  QSN097  CAS45773  BAC85171  BAC85171  BAC8517  BAC8517  BAC65017  BAC65017  BAC65011  BAC05012  BAC05012  BAC05013
	EWVSSMSSSSYI	ngth 471; als 3; aEWVAYISSGG	4 e	naratne P.H., J., Hulyk S.W. B.R.A., S., Sanchez A. s., Sanchez A. ard G.G., utterfield Y.S, , Schein J.E., ull-length hum	Schuler G.D., Bhat N.K., Hsieh F., ong L., Scheetz T.E., Prange C., prange C., Mullahy S.J.	); Buteleostomi	Aahlaja37 homo sapi Aahlaja37 homo sapi Bac85175 homo sapien Cae45773 homo sapien Cae45773 homo sapi Bac85171 homo sapi Bac8525 homo sapien Qzzp5 homo sapien Aah62336 homo sapi Bac85117 homo sapi Bac8514 homo sapi Bac8514 homo sapi Bac85012 homo sapi

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XX MEDLINE=22388257; PubMede=124777932;

XX MEDLINE=22388257; PubMede=124777932;

XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Altechul S.F., Jordan H., Moore T., Max S.I., Wannin G.M., Hong L.,

XX Altechul S.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

XX Altechul S.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

XX Altechul S.F., Jordan H., Moore T., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altechul S.F., Schein J.F., Schein J.E.,

XX Altechul S.F., Schein J.F.,

XX Altechul S.F., Schein J.F.,

XX Altechul S.F., Schein J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pri
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05-JUL-2004
05-JUL-2004
                                 Strausberg R.;
Submitted (DEC-2001) to the
EMBL; BC018747; AAH18747.1;
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like
                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
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         BC018747; AAH18747.1; -.
Pro; IPR003599; Ig.
Pro; IPR007110; Ig-like.
Pro; IPR003597; Ig_c1.
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1. Acad. Sci. U.S.A. 99;
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Primates;
      Ig.
Ig-like.
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Last annotation update)
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                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGV; 1.
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Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556
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02-MAR-2004
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MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.
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Homo sapiens (Human).
Eukaryota; Metazoa; C
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TISSUE=Primary B-Cells;
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Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; C:
Mammalia; Eutheria; Primates; C:
NCBI TaxID=9606;
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SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
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7; Mismatches
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D.,

RA Altschall S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschanko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K.J., Toshiyuki S., Carninci P., Prange C.,

RA Staplèton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wedlin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Arnes S. T. Marra M.A.
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Best Local S
Matches 419
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Submitted (DEC-2002) io the EMBL/GenBa:
EMBL; BC041037; AAH41037.1; -.

InterPro; IPR003599; Ig -11.

InterPro; IPR003107; Ig c1.

InterPro; IPR003597; Ig c1.

InterPro; IPR003597; Ig -MHC.

InterPro; IPR003596; Ig -WHC.

InterPro; IPR003596; Ig -WHC.

Iften; PF07654; C1-set; 3.

Pfam; PF00047; IG; 2.

SMART; SM00409; IG; 2.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS50835; IG LIKE; 4.
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"Generation and initial analysis
and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99;
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Pred. No. 6.9e
10; Mismatches
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Best Local S
Matches 419
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XX MEDIINE-2238257, PubMed-12477932;
XX MEDIINE-2238257, PubMed-12477932;
XX MEDIINE-2238257, PubMed-12477932;
XX MEDIINE-2388257, PubMed-12477932;
XX MEDIINE-2388257, PubMed-12477932;
XX MEDIINE-2388257, PubMed-12477932;
XX MITCHINE-2388257, PubMed-12477932;
XX MITCHINE-2388257, PubMed-12477932;
XX MITCHINE-2388257, May Structure C.F., Bhat N.K.,
XX MITCHINE-2388257, MAX Structure C.F., May Structure C.F., Mullahy S.J.,
XX MITCHINE-2388257, MARCKETHAN K.J., Malek J.A., Gunarathe P.H.,
XX MITCHINE-2388257, MARCKETHAN K.J., Malek J.A., Gunarathe P.H.,
XX MITCHINE-2388257, MARCKETHAN M.F., Garcia A.M., Gay L.J., Hulyk S.W.,
XX MITCHINE-2388257, MARCKETHAN M.F., Madan A., Rodrigues S., Sanchez A.,
XX MITCHINE-2388257, MARCKETHAN M.F., Shetchan J.W., Green E.D., Dickeon M.C.,
XX MITCHINE-2388257, MARCHINE-2388257, MARCHINE-238825, MARCHINE-2388257, MARCHINE-238825, MARCHINE-238825, MARCHINE
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02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
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SEQUENCE 478 AA; 52666 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2002) to the EMEL; BC041037; AAH41037.1; -.
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Proc. Natl. Acad. Sci. U.S.A.
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Mammalia; Eutheria;
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Pred. No. 6
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Best Local S
Matches 416
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THE GERMAN HUMAN CDNA CONSORTIUM;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C.,
Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ dat
EMBL; BX649947; CAE45972.1; -.
InterPro; IPR003599; Ig.-1:
InterPro; IPR003597; Ig.-1:
InterPro; IPR003597; Ig.-1:
InterPro; IPR003597; Ig.-1:
InterPro; IPR003596; Ig. WHC.
InterPro; IPR003056; Ig. WHC.
InterPro; IPR003596; Ig.-1:
InterPro; IPR003596; Ig.-1:
INTERPO; IPR003196; Ig.-1:
INTERPO; IPR003196; Ig.-1:
INTERPO; IPR003196; Ig.-1:
INTERPO; IPR00409; IG.:
SMART; SM00409; IG.:
SMART; SM00409; IG.:
SMART; SM00409; IG.:
PROSITE; PS50835; IG.LIKE; 4.
PROSITE; PS50835; IG.LIKE; 4.
PROSITE; PS50939; IG. LIKE; 4.
PROSITE; PS60290; IG. MHC; UNKNOWN_2.
SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein DKFZp686G11190.
Name=DKFZp686G11190;
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Pred. No. 7.4e
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AVLÓSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
                    AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
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CAE45972;
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Lauber J., Bahr A., Mewes H.W., Weil B., Amid
Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ
EMBL, BX640947; CAE45972.1; -.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence up
02-MAR-2004 (TrEMBLrel. 27, Last annotation
Hypothetical protein DKFZp686G11190.
DKFZP686G11190.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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                                                                PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                                                                                                                                 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
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3; Mismatches 20; 1
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Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ dat
EMBL; BX640853; CAR45920.1; -
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig. 11ke.
InterPro; IPR003597; Ig. Cl.
InterPro; IPR003597; Ig. MHC.
InterPro; IPR003595; Ig. W.
Fam; PP00654; Cl.-set; 3.
Pfam; PP0047; ig; 4.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 3.
SWART; SW00409; IG; 1.
SWART; SW00409; IG; 1.
RPROSITE; PS00290; IG-MHC; UNKNOWN_2.
Hypothetical protein.
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Q5MZV7;
Q5-JUL-2004 (TrEMBLrel
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Q5-JUL-2004 (TrEMBLrel
Q5-JUL-2004 (TrEMBLrel
Hypothetical protein D
Name=DKFZp686C11235;
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THE GERMAN HUMAN CONA CONSORTIUM;
THE GERMAN HUMAN CONA CONSORTIUM;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
protein DKFZp686C11235.
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Primates;
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                               BAC85232 PRELIMINARY;
BAC85232;
02-MAR-2004 (TrEMBLrel. 2:
02-MAR-2004 (TrEMBLrel. 2:
02-MAR-2004 (TrEMBLrel. 2:
CDNA FLJ26265 fis, clone
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TISSUB=Human small intestine;
TISSUB=Human small intestine;
Bloecker H., Boecher M., Mewes H.W., Weil B.,
Bloecker H., Boecher M., Mewes H.W., Weil B.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ
EMBL; BX640853; CAE45920.1; -.
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02-MAR-2004 (TIEMBLrel. 27, Created)

02-MAR-2004 (TIEMBLrel. 27, Last sequence up

02-MAR-2004 (TIEMBLrel. 27, Last annotation

Hypothetical protein DKFZp686C11235.

DKFZP686C11235.
 Eukaryota;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primata; (
             Homo
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EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY
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19 DMC05516, highly similar t
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 Craniata;
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Best Local Similarity
Matches 410; Conserv
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Q6GMW7;
05-JUL-2004 (TrRMBLrel. 2
05-JUL-2004 (TrRMBLrel. 2
05-JUL-2004 (TrRMBLrel. 2
MEDIJINE=32388257; PubMed=12477932;
MEDIJINE=32388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
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TISSUB-Dermoid tumor;

TISSUB-Dermoid tumor;

Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,

Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.

Hata H., Nakagawa K., Mizuno S.,

Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., S

Kawakami B., Nagai K., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AK129776; BAC85232.1; -.

EMBL; AK129776; BAC85232.1; -.

SEQUENCE 472 AA; 51212 MW; O1BF215F99809164 CRC64;
                                                                                                                                                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Mecazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                         TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLGGPSVFLFPPXPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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Pred. No. 1.
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                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae
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on update)
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                                                    C.M., Schuler G.D.
C.F., Bhat N.K.,
g.J., Haieh F.,
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Query Match
Best Local S
Matches 415
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, BC073782; AAH73782.1; -.

R Interpro; IPR003599; Ig.
R Interpro; IPR003599; Ig.-like.
R Interpro; IPR003597; Ig.-like.
R Interpro; IPR003597; Ig.-like.
R Interpro; IPR003596; Ig_wHC.
R Interpro; IPR003596; Ig_w.
R Interpro; IPR003596; Ig_v.
R Pfam; PF07654; Cl-set; 3.
R Pfam; PF00047; ig; 4.
R PFAMT; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 1.
R SMART; SM00406; IGv; 1.
R PROSITE; PS00835; IG_MHC; UNKNOWN_2.

W Hypothetical protein.

M SEQUENCE 475 AA; 51987 MW; 2AIFE55D736860F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones S.J., 'Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Similarity 91.0%;
15; Conservative 1
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                                                                                                                           PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                                                                                                  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                     PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                     VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                    REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
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                                                                                                                                                                                                                                                                                                          PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 2188.5; DB 2;
; Pred. No. 2.3e-134;
11; Mismatches 23;
                                             449
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RC TISSUE-Peripheral Nervous System;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Wares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Guellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robestelm M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Wonley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Tone S.T. Marra M.A.:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BCO72419; AAH72419:1;
InterPro; IPRO03599; Ig.-1ike.
InterPro; IPRO03599; Ig.-1ike.
InterPro; IPRO03597; Ig.-1ike.
InterPro; IPRO03597; Ig.-1ike.
InterPro; IPRO03597; Ig.-1ike.
InterPro; IPRO03596; Ig.-MHC.
InterPro; IPRO03596; Ig.-1ike.
Pfam; PF07654; C1-set; 3.
Pfam; PF007654; C1-set; 3.
PFAMRT; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; MHC; UNKNOWN 2.
PROSITE; PS50835; IG MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50853 MW; 53EBOBCEDE81076E CRC
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Q6IN78;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.;
"Generation and initial analysis of more and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Peripheral Nervous System;
Strausberg R.;
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179
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415; Conserv
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                                                     SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
                                                                                   SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
                                                                                                                                                                 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---GNYVVPAAPWGQGTLVTVS
                                                                                                                                                                                                        SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDS--WGQGTLLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JUN-2004) to the
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27,
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Pred. No. 2.9e
11; Mismatches
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Best Local S
Matches 414
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-Human rectum tumor;
THE GERMAN HUMAN CDNA CONSORTIUM;
THE GERMAN HUMAN CONSORTIUM;
THE GERMAN HUMAN CONSORTIUM;
THE GERMAN HOME AND THE MEMBL/GENBANK/DDBJ date with the death of the EMBL/GENBANK/DDBJ date with the first of the f
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
Hypothetical protein DKFZp686P15220.
Name=DKFZp686P15220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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    LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE
                                                                                                                                          EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY
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Primates;
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%; Pred. No. 2.9e-
13; Mismatches
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Best Local Similarity
Matches 414; Conserv
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02-MAR-2004
02-MAR-2004
02-MAR-2004
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Submitted (AUG-2003) to the
EMBL; BX640627; CAB45781.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae;
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Wambutt R., Heubner D., Mewes H.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 2187; DB 2;
; Pred. No. 2.9e-134;
13; Mismatches 21;
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SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                                                      EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                          LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
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                                                                                EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
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UZ-MAR-2004 (TEMBLrel. 27, Last sequence update)
Hypothetical protein DKFZp686P15220.
BKFZp686P15220.
Homo gamester update)

Euteleostomi;

Amid databases CRC64; Length G., Indels Osanger 472; 9 Gaps

EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV SDSVKGRFTISRDNSKNTLYLOMRSLRAEDSAVYFCTRVKLGT---YYF--DSWGQGTLL LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE LQSSGLYSLSSVVTVPSSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP LLGGPSVPLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 198 138 115 355 295 258 235 79 415 378 318

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RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12.477932;

RX MEDLINE=2388257; PubMed=12.477932;

RX Altausner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

RA Altausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altausner R.D., Collins F.S., Wagner A.A., Rubin G.M., Hong L.,

RA Altausner R.D., Jordan H., Moore T., Max S.I., Wang J., Heiden F.,

RA Altausner R.D., Jordan H., Moore T.A., Rabin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T.A., Casavant T.L., Scheetz T.E.,

RA Lichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Alnes S.J., Marra M.A.:
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Best Local S
Matches 414
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Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006402; AAH06402.1; -.
Hypothetical protein.
SEQUENCE 479 AA; 52281 MW; D74E0C89082A9788 CRC64;
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S.J., Marra M.A.; "Jones S.J., Marra M.A.; "Generation and Initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                          HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
                                                                                                                                     GQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
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                                      HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCP
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                                                       VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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Search completed: December 23, 2004, 19:04:37 Job time : 163.904 secs

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1 DIQMTQSPSSLSASVGDRVT.....HQYSKLPWTFGQGTKVEIKR
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Anti-VEGF
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Ganglioside; GD3; complementarity determining region; CDR; antibody;

110 2 AAW70675 110 5 ABP61244 108 2 AAW70618 108 5 ABP61187 108 8 ADG31798 108 8 ADG31798 110 3 AAB05897 110 3 AAB05897 110 3 AAB05897 110 2 AAW70623 107 2 AAW70627 110 2 AAW70677 110 3 AAB13380 110 5 ABP61256 110 5	AAB81988; 03-JUL-2001 (first )	SSULT 1 .B81988 , AAB81988 standard; p:	0.	500	500 88.0	88.0	500 88.0	500 88.0	500 88.0	500 88.0	501 88.2	501 88.2	501 88.2	503 88.6	503 88.6	503 88.6	503 88.6	503 88.6	503 88.6	503 88.6	504 88.7	504 88.7	
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Query Match 100.0%; Score 568; DB 4; Best Local Similarity 100.0%; Pred. No. 1.2e-35; Matches 108; Conservative 0; Mismatches 0;
                                                                       The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                                                                                       New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
                                                Sequence 108
                                                                                                                                                                                                                                                                                                             30-SEP-1999; 99JP-00278291
06-APR-2000; 2000JP-00105088
                                                                                                                                                Claim 22; Page 172-173; 183pp; Japanese.
                                                                                                                                                                                                                                       WPI; 2001-266143/27.
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                        ABU11011 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
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06-APR-2000; 2000JP-00105088
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                                                                                                                                                                                                                                                                                         DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shitara K,
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific antibody related
                        protein; 108
                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                          Score 568; Db 4;
Pred. No. 1.4e-35;
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RESULT 4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reactions, particularly to relieve problems of side-effects during the conventional single administration. This sequence represents a protein associated with the anti- ganglioside GD3 antibody
                                                                                                                                                03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drugs containing genetically-modified antibody against ganglioside GD3, its fragment, immunocompetent cell activators or/and antitumor agents i combination, applicable in treating malignant tumor like melanoma.
                                                          Synthetic
                                                                                              Ganglioside;
                                                                                                                       Ganglioside GD3 specific antibody related protein #3.
                                                                                                                                                                                                 AAB81994
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 100; 121pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-067410/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2001; 2001JP-00097483
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                                   WO200123432-A1
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                                                                                                                                                                                                                                                                                                                                                                                                              108 AA;
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                                                                                                                                                                                                                                                             RESGGGGGGTDYTLTISSLOPEDIATYFCHOYSKLPWTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                             DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAPKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                              GD3;
                                                                                                                                                (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                              complementarity determining region; CDR; antibody;
                                                                                                                                                                                                protein;
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Pred. No. 3.4e-35;
0; Mismatches 1
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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically with ganglioside GD3. The antibody and its derivatives useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplifica of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
New human type complementation-determining region-transplanted and derivatives against ganglioside GD3, useful in diagnosis ar
                                                                                                     30-SEP-1999; 99JP-00278291.
06-APR-2000; 2000JP-00105088.
                                                                                                                                                          05-APR-2001
                                                                                                                                                                                                                              Ganglioside;
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06-APR-2000; 2000JP-00105088.
                                                              Hanai N,
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                                                                                   (KYOW)
                                         2001-266143/27.
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                                                                                  куома накко косуо
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                                                                                                                                                                                                                                                                                                                standard; protein; 128
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                                                                                                                                                                                                                                                                                                                                                                    RESGGGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGQGTKVEIKR
                                                           Shitara K,
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                                                                                                                                                                                                                             GD3; complementarity
                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                  specific antibody related protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%;
                                                                                                                                                                                                                                                                        entry)
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                                                               Nakamura
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Pred. No. 4.7e-35;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specifically with ganglioside GD3. The antibody and its derivatives useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                    The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                        New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
                                                                                                                                                                                                                                     30-SEP-1999;
06-APR-2000;
 Sequence 128
                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                   Ganglioside;
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                                                                                     Example 1;
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                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO
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DB; AAF86895.
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                                                                                                                                                                                            Shitara K,
                                                                                     Page 153;
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2000JP-00105088.
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98.1%;
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Pred. No. 1.3e-34;
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Query Match

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Best Local S
Matches 104
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AAB81995 standard; protein; 128
                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
                                                                                                                                                                                                                                                                                                                                   Sequence 108 AA;
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06-APR-2000; 2000JP-00105088
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Pred. No. 3.9e-34;
1; Mismatches 3
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                                                        Synthetic
                                                                                             Ganglioside; cancer.
                                                                                                                                                      Ganglioside GD3 specific antibody related protein #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 128 AA;
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                                                                                                                 complementarity determining region;
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                           WPI; 2001-266143/27.
N-PSDB; AAF86912.
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                                                                                              Shitara K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 11
AABB1992
ID AABB1
XX AABB1
AC AABB1
XX AABB1
XX Gangl
XX Gangl
XX Gangl
XX Gangl
XX Gangl
XX Gangl
XX Cance
XX Cance
XX ABB1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                                                                                                                                                      New human type complementation-determining region-transplanted antibody derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1999;
06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ganglioside;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 128
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB81992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB81992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (КУОМ ) КУОМА НАККО КОСУО КК
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200123432-A1
                                                                                                                                                                                                                                                                                                                                                               2001-266143/27.
DB; AAF86892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIQMTQSASSLPASVGDRVTITCSASQDISNYLNWYQQKPGKAVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-00278291
2000JP-00105088
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128
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.1e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                        and therapy
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The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

Example 1; Page 150-151; 183pp; Japanese

Sequence 128 AA;

Length 128

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AABB1990
ID AABB1
XX AABB1
XX AABB1
XX AABB1
XX Gangl
XX 
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                                                                                                                                                                                                             Query Match
Best Local S
Matches 96
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Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                          Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 174-175; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1999; 99JP-00278291.
06-APR-2000; 2000JP-00105088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ganglioside; GD3; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2000; 2000WO-JP006774.
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61
                                 61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                             96;
                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                            Similarity
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                                                                                                      DIOMTOTASSLPASLGDRVTISCSASODISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shitara K,
                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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                                                                                                                                                                                                                                      90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
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Pred.
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Pred. No. 7.3e-33;
2; Mismatches 5
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                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                           e 514; DB 4; Le
. No. 1.4e-31;
ismatches 5;
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                                                                                                                                                                                                                                                             Length 108,
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RESULT 13

Key

Location/Qualifiers

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ABUI1013
ID ABUI1
XX ABUI
XX ABUI
XX Modil
XX Modil
XX Modil
XX MO2C
XX MUS
XX WO2C
XX WOI
XX WPI
XX Clas
XX CC Sep
SQ Seq
SQ Seq
SQ Seq
                                                                                                                                                                                                            RESULT 14
AAB01628
ID AAB01
X S X F X B X B X S X F
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Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reactions, particularly to relieve problems of side-effects during the conventional single administration. This sequence represents a protein associated with the anti- ganglioside GD3 antibody
                             Mug
                                                                                                              Murine
                                                                                                                                                                                                            AAB01628 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drugs containing genetically-modified antibody against ganglioside GD3, its fragment, immunocompetent cell activators or/and antitumor agents i combination, applicable in treating malignant tumor like melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shitara K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ganglioside GD3;
                                                                            Mouse;
                                                                                                                                               07-DEC-2000
                                                                                                                                                                              AAB01628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001; 2001JP-00097483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2002; 2002WO-JP003170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified ganglioside GD3 antibody
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                                                               humanised antibody.
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                                                                            immunoglobulin;
                                                                                                             immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                            DIQMTQTASSLFASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
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                                                                              chain; light chain; variable
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 514; DB 6;
Pred. No. 1.4e-31;
7; Mismatches 5
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Matches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized chimera antibody KM-871 useful for treating cancer, comprises variable region of mouse monoclonal antibody, reactive with ganglioside and human antibody constant region.
                                                                                                                              Ganglioside; GD3; complementarity determining region; CDR; antibody;
cancer.
                                                                                                                                                                  Ganglioside GD3 specific antibody related protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 128 AA;
 30-SEP-1999;
                         29-SEP-2000; 2000WO-JP006774.
                                                    05-APR-2001.
                                                                           WO200123432-A1
                                                                                                      Mus musculus
                                                                                                                                                                                             03-JUL-2001
                                                                                                                                                                                                                                               AAB81976
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18-SEP-1992;
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 99JP-00278291
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92EP-00116026.
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/label= signal_peptide
21. .128
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                                                                                                                                                                                                                                                                                                                                                                                                 New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                                                                                                     Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 140; 183pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                      activity in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-266143/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanai
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                                                                         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR
                                                                                                              21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                       RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
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             2004,
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7; Mismatches 5
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US-09-225-322B-10
US-09-264-304-19
US-09-764-304-19
US-09-764-304-19
US-09-764-304-19
US-09-765-059-3
US-08-649-100-33
US-08-649-100-33
US-08-652-558-2
US-09-406-52-558-2
US-09-406-52-558-2
US-08-437-642B-17
US-08-686-17
US-08-705-392A-17
US-09-705-392A-17
US-09-934-373C-25
US-09-940-18A-2
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US-09-940-18A-2
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US-09-940-58A-2
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480 84.5 214 3 US-09-460-587-2 Sequence 2, 480 84.5 214 4 US-09-940-166A-2 Sequence 2, 480 84.5 214 5 PCT-US93-07832-40 Sequence 40 480 84.5 233 2 US-07-934-373C-25 Sequence 25	480 84.5 214 2 US-08-788-800-11 Sequence 10 480 84.5 214 3 US-08-437-642B-40 Sequence 40 480 84.5 214 3 US-09-097-309-2 Sequence 2, 480 84.5 214 3 US-09-097-178-2 Sequence 2,	480 84.5 107 5 PCT-US93-07832-17 Sequence 17 480 84.5 109 2 US-07-934-373C-47 Sequence 47 480 84.5 109 3 US-08-437-642B-47 Sequence 47 480 84.5 109 3 US-08-437-642B-47 Sequence 47	480 84.5 107 3 US-08-437-642B-17 Sequence 17 480 84.5 107 4 US-08-146-206C-17 Sequence 17 480 84.5 107 4 US-09-705-666-17 Sequence 17 480 84.5 107 4 US-09-705-392A-17 Sequence 17	5 503 88.6 110 4 6 491 86.4 108 3 7 487 85.7 127 3 8 484 85.2 214 1 9 481 84.7 110 4 9 480 84.5 107 2	514 90.5 128 4 US-09-225-322B-10 Sequence 10 514 90.5 128 4 US-09-225-322B-19 Sequence 19 514 90.5 128 4 US-09-764-304-19 Sequence 19 514 90.5 128 4 US-09-764-304-19 Sequence 19	SUMMARIES  It Query  O. Score Match Length DB ID  Description	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	base: Issued_Patents_AA:*  1: /cgn2_6/ptodate/1/iaa/5A_COMB.pep:*  2: /cgn2_6/ptodate/1/iaa/5B_COMB.pep:*  3: /cgn2_6/ptodate/1/iaa/6A_COMB.pep:*  4: /cgn2_6/ptodate/1/iaa/6B_COMB.pep:*  5: /cgn2_6/ptodate/1/iaa/6B_COMB.pep:*  6: /cgn2_6/ptodate/1/iaa/backfIles1.pep:*	-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	mum DB seq length: 0 mum DB seq length: 2000000000	l number of hits satisfying chosen parameters: 478139	ched: 478139 segs, 66318000 residues	ing table: BLOSUM62 Gapop 10.0 , Gapext 0.5	e: US-10-089-500-54 ect score: 568 ence: 1 DIQMTQSPSSLSASVGDRVTHQYSKLPWTFGQGTKVEIKR 108	on: December 23, 2004, 18:46:39 ; Search time 7.13276 Seconds (without alignments) 1004.148 Million cell updates/sec	rotein - protein search, using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
RESULT 2 US-09-225-322B-19 ; Sequence 19, Application US/09225322B	Qy 61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108	Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60	Query Match 90.5%; Score 514; DB 4; Length 128; Best Local Similarity 88.9%; Pred. No. 1.2e-43; Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;	; LENGTH: 128 ; TYPB: PRT TYPB: PRT ; ORGANISM: Artificial Sequence ; FEATURE: ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641 US-09-225-322B-10	>> >31	; PRIOR APPLICATION NUMBER: US 08/292,178 ; PRIOR FILING DATE: 1994-08-17 ; PRIOR APPLICATION NUMBER: US07/947,674 ; PRIOR FILING DATE: 1992-09-17 • PRIOR FILING DATE: 1992-09-17	; PRIOR APPLICATION NUMBER: US 08/454,680 ; PRIOR PILING DATE: 1995-05-31 ; PRIOR APPLICATION NUMBER: US 08/408,133 ; PRIOR FILING DATE: 1995-03-21	APPLICANT: HANAI, NOBUO APPLICANT: HASEGAWA, MAMORU APPLICANT: MIYAJI, HICOMASA APPLICANT: MIYAJI, HICOMASA APPLICANT: KUWANA, YOSHIHISA TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY FILE REFERENCE: 249-101 CURRENT APPLICATION NUMBER: US/09/225,322B CURRENT FILING DATE: 1999-01-05	US-09-225-3228-10 ; Sequence 10, Application US/09225322B ; Patent No. 6437098 ; GENERAL INFORMATION: ; APPLICANT: SHITARA, KENYA	RESULT 1	ALIGNMENTS	83.6 126 1 US-08-137-117D-71 Sequence 7.	475 83.6 111 1 US-08-137-117-67 Sequence 67.	39 479 84.3 107 1 US-08-458-516-8 Sequence 8, Appli 40 476 83.8 107 3 US-09-254-189-1 Sequence 1, Appli 40 476 83.6 108 3 US-09-254-189-3 Sequence 3, Appli 41 475 83.6 108 3 US-08-574-899-3 Sequence 3, Appli 42 47 87 87 108 4 US-08-748-98-3 Sequence 3, Appli 42 47 87 87 108 4 US-08-748-788-3 Sequence 3, Appli 42 47 87 88 108 4 US-08-748-788-3 Sequence 3, Appli 48 18 18 18 18 18 18 18 18 18 18 18 18 18	480 84.5 237 3 US-09-422-712B-2 Sequence 2, 480 84.5 237 3 US-09-607-756-2 Sequence 2, 480 84.5 237 3 US-09-460-587-6 Sequence 6, 480 84.5 237 3 US-09-460-587-6 Sequence 6,	480 84.5 233 5 PCT-US93-07832-25 Sequence 25 480 84.5 237 3 US-09-097-309-6 Sequence 6, 480 84.5 237 3 US-09-097-171A-10 Sequence 10	480 84.5 233 3 US-08-437-642B-25 Sequence 480 84.5 233 4 US-08-146-206C-25 Sequence 480 84.5 233 4 US-09-705-686-25 Sequence 480 84.5 233 4 US-09-705-392A-25 Sequence

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                                                                                                                                                                                                         FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
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APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYALI, HIROMASA
APPLICANT: MIYALI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Appli
Patent No. 6495666
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HOCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT APPLICATION NUMBER: US 08/454,680
PRIOR APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                    EARLIER APPLICATION NUMBER: US 08/292,176
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER:
                                                                                                      EARLIER APPLICATION NUMBER: US07/947,674 EARLIER FILING DATE: 1992-09-17
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PRIOR FILING DATE: 1992-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: light chain OTHER INFORMATION: variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DIQWIQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 514; DB 4;
Pred. No. 1.2e-43;
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US-09-764-304-19
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; PEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-10
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CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 07/947,674
EARLIER APPLICATION NUMBER: US 07/947,674
                                                                                                                                                                                                                                                                                       SEQ ID NO 19
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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LENGTH: 128
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Patent No. 6495666
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                 OTHER INFORMATION: light chain OTHER INFORMATION: variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                          Local
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                                                                                                                                                        96;
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                                                                                                                                                                          Similarity
                                                                       DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                               DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                                                                                                                    Score 514; DB 4;
Pred. No. 1.2e-43;
7; Mismatches 5
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RESULT 5 US-09-440-781-94

Sequence 94, Application US/09440781 Patent No. 6632926

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CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Patent No. 606884
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APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yvonne Man-yee Chen et al. TITLE OF INVENTION: ANTIBODY VARIANTS FILE REFERENCE: P1469R1
                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acid
                                                                                                                                                                                                                                                                                                         ZIP: 2/21-
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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ORGANISM: artificial sequence
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                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE DOCKET NUMBER: 50356-151
                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OKUMURA, KO
APPLICANT: NAKATA, MOTOMI
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
                                                                                                                     TELEPHONE: 703-518-5100
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: >> CITY: Alexandria
                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                 CLASSIFICATION:
              STRANDEDNESS:
                                                                                                                   TELEPHONE:
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                               amino acid
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                                            108 amino acids
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linear
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Pred. No. 1.2e-42;
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                                                                                                                      Best Loc
Matches
                                                                                                                                                  Query Match
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Patent No. 6
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                                                                                                                                                                                                                                                                                     IELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                  NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 11:
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VASQUEZ, MAXIMILIANO
                                                                                                                                     Local Similarity
                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
 18
                   61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
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                                                                                                                      92;
                                                                              1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                          amino acid
                                                         DIQMTQSPSTLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
RFSGSGSGTNYTLTISSLQPDDFATYFCQQGSTLPWTFGQGTKVEVK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATUSUE, TOMOKAZU
NAGATA, SHIGEKAZU
CO, MAN SUNG
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIRAKAWA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                             single
                                                                                                                                     85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-FAS LIGAND ANTIBODY AND ASSAY METHOD USING THE ANTI-FAS LIGAND ANTIBODY
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                                                                                                                   Score 487; DB 3;
Pred. No. 5.6e-41;
6; Mismatches 9
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Pred. No. 1.9e-41;
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                                                                                                                                                  Length 127;
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APPLICANT: L...

APPLICANT: TSO, J...

APPLICANT: TSO, J...

ITITLE OF INVENTION: Humanı...

ITITLE OF INVENTION: GPIIB/IIA

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                             뫄
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                                                                                                                                                                                                                            US-09-440-781-95
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                                                                                                                                                                  Sequence 95, Applicate Patent No. 6632926 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS:
SEQ ID NO 95
LENGTH: 110
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                         CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
                                                                                                              APPLICANT: Yvonne Man-yee Chen et al. TITLE OF INVENTION: ANTIBODY VARIANTS FILE REFERENCE: P1469R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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o. 5777085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 85.2%;
Similarity 83.3%;
                                                                                                                                                                                                                                                                                                  RFSGSGSGTDYTLTISSLQPDDFATYFCQQGNTLPWTFGQGTKVEVKR 108
                                                                                                                                                                                                                                                                                                                                                                         DIOMTOTPSTLSASVGDRVTISCRASODINNYLNWYQQKPGKAPKLLIYYTSTLHSGVPS
                                                                                                                                                                                                         Application US/09440781
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Pred. No. 2e-40;
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US-07-934-373C-17
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Best Local S
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Matches
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                                                                                       Query Match
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APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
                                                                                                                                                                                                                                               FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US92/
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/715272
APPLICATION UNMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P070
                                                                                                                                                                                          TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wilpatin (Genentech)
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: IT NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
                                                                                                                                   TOPOLOGY:
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                                                                                                                                                            ENGTH:
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RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR
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San Francisco
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                                                                                                                                  Linear
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81.5%;
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                                                                        84.5%;
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Pred. No. 1.9e-40;
2; Mismatches 8
                                                           Score 480; DB 2;
Pred. No. 2.3e-40;
4; Mismatches 11;
                                                                                      Length 107;
                                                            Indels
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US-08-437-642B-17
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US-08-652-558-2
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Patent No. 6054297

GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                     Sequence 17,
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Patent No. 5861155
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/652,558
FILLING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILLING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4
COMPUTER: ISM PC compatible
OPERATING-SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LIN, AUG
TITLE OF INVENTION:
TITLE OF INVENTION:
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Local Similarity 86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: 811
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                    61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEI 106
                                                                                                                                                                                                                                                                                                                                                                                                              92;
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                                                                                                                                                                   Application US/08437642B
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ON: HUMANIZED ANTIBODIES
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Matches
                                                                                                                                                                                                                                              Sequence 17, Application US/08146206C Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Mal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIPICATION DATA:
APPLICATION NUMBER: 07/934373
APPLICATION NUMBER: 07/934373
APPLICATION NUMBER: 08/146206
PRIOR APPLICATION NUMBER: 08/146206
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION NUMBER: 08/146206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION. FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
PILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715
PILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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ADDRESSEE: Gence.
Therefore 1 DNA Way
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
                                                                                                       COUNTRY: U
                                                                                                                                           CITY: South San Francisco
STATE: California
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California
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WinPatin (Genentech)
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for Making Humanized Antibodies
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Pred. No. 2.3e-40;
4; Mismatches 11
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CURRENT APPLICATION DATA:

FILING DATE:

PPLICATION NUMBER: US/08/146,206C TLING DATE: 17-No. 6407213-1993

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US-09-705-686-17
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GENERAL INFORMATION:
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                  INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
07/715272
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M:

REGISTRATION NUMBER: 40,378

REGISTRATION INFORMATION:

TELEPHONE: 650/225-1994

TELEPHONE: 650/225-1994
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                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Carter, Paul J.

Presta, Leonard G.

TITLE OF INVENTION: Method for Making Humanized Antibodies
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
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CITY: South San Francisco
STATE: California
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                TELEFAX: 650/952-9881
N FOR SEQ ID NO: 17:
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Pred. No. 2.3e-40;
4; Mismatches 11
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RESULT 15
US-09-705-392A-17
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                                                                                                                Matches
                                                                                                                                  Query Match
Best Local :
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Best Local Similarity
                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705,392A

FILING DATE: 02-No. 6719971-2002

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
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 61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
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                                                                           1 DIOMIOSPSSLSASVGDRVITICSASODISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                                                                                                  Similarity
                             TYPE: Amino Acid TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                     LENGTH: 107 amino acids
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                                                                                                            84.5%; Score 480; DB 4; Length 107; 86.0%; Pred. No. 2.3e-40; tive 4; Mismatches 11; Indels
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86.0%;
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Pred. No. 2.3e-40;
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61 RPSGSGSGTDYTLTISSLQPEDFATYYCQQCNTLPWTFGQGTKVBIK 107

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Search completed: December 23, 2004, 19:08:00 Job time: 17.1328 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                    Score
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568
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Length
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m2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
m2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USOA_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USOA_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USOC_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*
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6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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    US-09-056-160B-103

US-10-234-671-101

US-09-056-160B-100

14 US-10-234-671-100

15 US-10-011-125-2

US-09-056-160B-15

US-10-234-671-15
                                                                                                                                                 US-09-764-304-10
US-09-764-304-19
4 US-10-265-713-10
4 US-10-265-713-19
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Sequence 10, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 10, Appl
Sequence 103, Appl
Sequence 101, Appl
Sequence 100, App
Sequence 100, App
Sequence 100, App
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
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## ALIGNMENTS

US-09-764-304-10

Sequence 10, Application US/09764304
Patent No. US20020026036A1
GENERAL INFORMATION:

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GENERAL LAFORMANIANA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER APPLICATION NUMBER: US08/940,133
EARLIER APPLICATION NUMBER: US08/940,133
EARLIER APPLICATION
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US-09-764-304-19
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CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 07/947,674
EARLIER APPLICATION NUMBER: US 07/947,674
                 Sequence 10, Application US/10265713
Publication No. US20030095964A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: MIYAJI, HIROMASA
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local &
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SEQ ID NO 19
LENGTH: 128
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Best Local
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APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
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APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: light chain OTHER INFORMATION: variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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KUWANA, YOSHIHISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 514; DB 9; Length 128; Pred. No. 7.1e-37;
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Pred. No. 7.1e-37;
7; Mismatches 5
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APPLICANT: HASKGAWA, MAMORU
APPLICANT: KUWANA, MAMORU
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1995-01-05
PRIOR FILING DATE: 1995-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-03-21
PRIOR PRILING DATE: 1995-03-21
PRIOR PRILING DATE: 1994-08-17
PRIOR PRILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1992-09-17
PRIOR PILING DATE: 1992-09-17
PRIOR PILING DATE: 1991-09-18
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FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR PILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 08/292,09-17
PRIOR APPLICATION NUMBER: US 08/292,076
PRIOR APPLICATION NUMBER: US 08/292,077
PRIOR APPLICATION NUMBER: US 08/292,076
PRIOR APPLICATIO
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                                                                                                                                                         SEQ ID NO 19
LENGTH: 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/10265713 Publication No. US20030095964A1
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                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 19
                                          ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                       TYPE: PRT
OTHER INFORMATION: Description of Artificial Sequence:light chain
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                                                                                                                     US-10-166-626-19
                                                                                                                                         RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 96
                                                        Sequence 19, Application US/10166626 Publication No. US20030166876A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US07/947,674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: MIYAJI, HIROMASA
PPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 128
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                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 514; DB 14; Pred. No. 7.1e-37; 7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 128;
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Best Local Similarity
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR PRIOR DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: light chain OTHER INFORMATION: variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYDE: 3.5 inch., 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA: 60/054,856
                                                                                           SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTI-VEGF ANTIBODIES NUMBER OF SEQUENCES: 131
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                   APPLICATION NUMBER: US/09/056,160B FILING DATE: 06-Apr-1998 CLASSIFICATION: 424
                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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FILING DATE: 1995-03-21
APPLICATION NUMBER: US 08/292,178
FILING DATE: 1994-08-17
APPLICATION NUMBER: US07/947,674
FILING DATE: 1992-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANT: KUWANA, YOSHIHISA
OF INVENTION: PROCESS F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 3-238375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
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                                                                                                                                                                                                                                                                                           1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                     Chen,
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Lowman, Henry B.
Chen, Yvonne M.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Wells, James A.
                                                                                                               WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baca, Manuel
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                                                                                                                                                                                                                                                                                                         Genentech,
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06-AUG-1997

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US-10-234-671-101
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SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 101, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                 INFORMATION FOR SEQ ID NO: 101:
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REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160

FILING DATE: 05-APR-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                 ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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STREET: 1 DNA WAY
STREET: 1 DNA WAY
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/234,671 FILING DATE: 03-Sep-2002
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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amino acids
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Pred. No. 2.5e-36;
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PRILING DATE: 06-Api---
PILING DATE: 06-Api---
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
PILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093F
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEPHONE: 650/922-9881
TELEPAX: 650/952-9881
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US-09-056-160B-100
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GENERAL INFORMATION:
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Best Local
                                                                                                                                        Matches
                                                                                                                                                                       Query Match
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                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baca, Manuel APPLICANT: Wells, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ANTI-VEGF ANTIBODIES NUMBER OF SEQUENCES: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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ADDRESSE: Ge...
There: 1 DNA Way
San Francisco
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Local Similarity 88.0%;
see 95; Conservative 7
                                                                                                                                                      Local
                                                                                                                                                                                                                                            TYPE: Amino Acid
                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
84
                                61
                                                                 24 DIQUTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQXPGKAPKLLIYPTSSLHSGVPS
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                                                                                       1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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Similarity 88.0%;
95; Conservative
                     RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
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RESGSGSGTDYTLTISSLOPEDFATYYCQQYSTVPWTFGQGTKVEIKR 131
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Lowman, Henry B.
Chen, Yvonne M.
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                                                                                                                                                                                                                                                                237 amino acids
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                                                                                                                                                                                                                             Linear
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Pred. No. 2.5e-36;
7; Mismatches 6;
                                                                                                                                      Score 507; DB 9;
Pred. No. 5.3e-36;
7; Mismatches 6
                                                                                                                                                                        Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/056160
APPLICATION NUMBER: 60/126446
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: 91093R2C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 650/952-9861
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
Sequence 2, Application US/10011125
Publication No. US20020142388A1
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST (
FILE REFERENCE: P1804R1
                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local S
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy diversely compatible computer: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
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                                                                                                                                                                                                                                              61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                      24 DIQLTQSBSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS
                                                                                                                                                                                                          84 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                               l Similarity
95; Conserv
                                                                                                                                                                                                                                                                                                                                   1 DIOMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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STATE: California
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Pred. No. 5.3e-36;
7; Mismatches 6;
                       STRAINS
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US-09-056-160B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. US20020032315A1 GENERAL INFORMATION:
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Best Local (
                                                                                                                                                           APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTI-VEGF NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                           TELEPHONE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94080
                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS
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Similarity 88.0%;
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Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
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                                                                                                           650/952-9881
                   Linear
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Query Match Best Local Similarity

88.9%;

Score 505; DB 9; Pred. No. 3.6e-36;

Length 107,

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US-10-234-671-15
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Best Local Similarity 88.8
Matches 95; Conservative
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TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/056160
PILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
PILING DATE: 03-Sep-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb !
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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61
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                  RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVBIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
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STATE: California
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STREET: 1 DNA Way
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Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inch, 1.44 Mb floppy disk
                                                                                                                       Score 505; DB 14; L
Pred. No. 3.6e-36;
Migmatches 6;
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                                                                                                                          6; Mismatches
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RESULT 15
US-10-234-671-103
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US-09-056-160B-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-056-160B-105
                                                                                                                                Sequence 103, Application US/10
Publication No. US20030190317A:
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 105, Application US/09056160B Patent No. US20020032315A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb flc

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,160E

FILING DATE: 06-Apr-1998

CLASSIFICATION UDMER: 60/054,856

APPLICATION NUMBER: 60/054,856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: HASAK, Janet E.

REGISTRATION UMBER: 28,616

REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650/225-18
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino Acids
TOPOLOGY: I.in.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 88.7%;
Local Similarity 87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                      Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                              61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  94;
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                                                                                                                                                                           Application US/10234671 o. US20030190317A1
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                                                                                            Wells, James A.
Presta, Leonard
                                                                          Lowman, Henry B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 504; DB 9;
Pred. No. 4.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 110;
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ADDRESSEE: Genentech, Inc.

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STREET: 1 DNA Way
CITY: South San Francisco
STRITE: GALIFORNIA
SOUNTRY USA

ZOUNTRY USA

ZOUNTRY USA

ZOUNTRY USA

COMPUTER RAMALE FORM:
MEDIUM TITE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER REAMALE FORM:
MEDIUM TITE: 3.5 Inch, 1.54 Mb floppy disk
COMPUTER REAMALE FORM:
MEDIUM TITE: 3.5 Inch, 1.54 Mb floppy disk
COMPUTER REAMALE FORM:
MEDIUM TITE: 3.5 Inch, 1.54 Mb floppy disk
COMPUTER REAMALE FORM:
MEDIUM TITE: 13 Mc florentech)
CURRENT APPLICATION DATA:
COMPUTER REAMALE FORM:
MAPLICATION WINDER: WIS/10/234,671
FILING DATE: 03-Sep-2002
FILING DATE: 03-Sep-2002
FILING DATE: 03-ARR-199
FRICK APPLICATION WINDER: 03-199
FRICK APPLICATION WINDER: 03-199
FRICK PAPLICATION WINDER: 03-199
FRICK PAPLICATION WINDER: 103-885.6
FILING DATE: 03-ARR-199
FRICK PAPLICATION WINDER: 144-637
FRICK PAPLICATION WINDER: 144-637
FRICK PAPLICATION WINDER: 144-637
FRICK PAPLICATION WINDER: 144-637
FRICK PARLET PAPLICATION WINDER: 145-37
FRICK PAPLICATION WINDER: 146-37
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FRICK PAPLICATION WINDER: 146-37
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<sup>This Page Blaink</sup> (uspto)

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
433	433	433	433	434	434	435	436	437	437	437.5	438	438	439	439	440
76.2	76.2	76.2	76.2	76.4	76.4	76.6	76.8	76.9	76.9	77.0	77.1	77.1	77.3	77.3	77.5
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ALIGNMENTS

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### A;Cross-references: GDB:136264 A;Map position: 2p12-2p12 C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1 c;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM> A;Contents: annotation; X-ray crystallography A;Note: the structure of the V region was determined by molecular replacement methods u R;Steiner, V; Chang, J.Y. FEBS Lett. 222, 6-10, 1987 A;Title: Chemical modification of the carboxyl groups of protein substrates enhances th A;Reference number: S02572; MUID:88005152; PMID:3115831 A;Contents: annotation C;Comment: This is a Bence Jones protein. A;Molecule type: protein A;Residues: 1-108 <SCH> A;Residues: 1-108 <SCH> A;Residues: 1-108 <SCH> A;Residues: 1-108 <SCH> A;Cross-references: UNIPROT:P01594 A;Note: the C region of this chain has the Inv (3) marker A;Pothlhammer, H.; Schiffer, M.; Epp, 70; Colman, P.M.; Lattman, E.E.; Schwager, P.; Ste Biophys. Struct. Mech. 1, 139-146, 1975 A;Title: The structure determination of the variable portion of the Bence-Jones protein A;Reference number: 390729; MUID:77022433; PMID:1234024 C;Accession: A91653; A01862; S02573 R;Schlechl, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972 A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, A;Reference number: A91653; MUID:72189444; PMID:5028201 A;Accession: A91653 Ig kappa chain V-I region (Au) - human C;Species: Homo sapiens (man) C;Date: 24-Apr-1984 #eequence revision 02-Jul-1998 #text\_change 09-Jul-2004 C;Accession: A91553; A01862; S02573 F;23-88/Disulfide bonds: #status predicted A;Gene: GDB:IGKV1 C;Genetics: Matches Query Match Local 61 61 RFSGGGSGTDYTLTISSLOPEDIATYFCHQYSKLPWTFGQGTKVEIKR **,** 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 92; Similarity RESGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIKR DIQMTQSPSSLSASVGDRVTITCQASQDISDYLMWYQQKPGKAPKLLIYDASNLESGVPS Conservative 84.5%; 5; Mismatches Score 480; DB 1; Pred. No. 1.7e-36; Length 108 Indels 108 108 Gaps 60

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RESULT 2

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Ig kappa chain V region (Py69) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_cC;Accession: G38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences A:Reference number: A38740; MUID:91177923; PMID:1706720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V region (Py20) - mouse (Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (;Date: 189-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004 (;Accession: A38740 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R. J. Biol. Chem. 266, 6607-6613, 1991 A;Title: Heavy and light chain variable region sequences and antibody proper A;Reference number: A38740; MUID:91177923; PMID:1706720 A;Accession: A38740
                                                                                                                                                                        RESULT
G38740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequence A;Reference number: A38740; MUID:91177923; PMID:170672
A;Accession: E38740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;19-93/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
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A; Residues: 1-111 < RUF>
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C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change
C;Accession: E38740
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Matches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                            RFSGSGSGTDYSLTISDLEPEDIATYYCQQYSKLPWTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                   DVQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                               84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                            11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Score 477; DB 2;
Pred. No. 3.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 479; DB 2;
Pred. No. 2.2e-36;
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A;Experimental source: MLR-lpr/lpr
A;Note: sequence extracted from NCBI backbone
R;Puccetti, A.; Koizumi, T.; Migliorini, P.; P
J. Exp. Med. 171, 1919-1930, 1990

A; Title:

immunoglobulin light

chain

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Lupus-prone

mouse ٠ :

induces

autoantibodies К.J.;

Barrett,

Schwart

e (NCBIP:60876)
Andre-Schwartz,

A;Status: preliminary; not A;Molecule type: nucleic ac A;Residues: 1-107 <KOI>

y; not compared leic acid

with

conceptual

A; Accession: B49026

A; Title: Molecular heterogeneity of auto-anti-idiotypic A; Reference number: A49026; MUID:91364791; PMID:1909645

R;Koizumi, T.; Puccetti, A.; Migliorini, Eur. J. Immunol. 21, 2185-2193, 1991

₽.;

Barrett,

K.J.; Schwartz,

R.S.

antibodies

in

MLR-lpr/lpr

mice

#text\_change

21-Jan-2000

mouse

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A;Accession: G38740
A;Status: preliminary; nucleic acid sequen
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:091WS9
A;Cross-references: immunoglobulin V region; im
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (1990 med.)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #ce:
C;Accession: C38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr.,
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequence.
A:Reference number: A38740; MUID:91177923; PMID:17067;
                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: in C;Keywords: hete F;19-93/Domain:
B49026
If kappa chain V region, anti-idiotypic monoclonal antibody C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_chaC;Accession: B49026; PLO220
C;Accession: B49026; PLO220
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C38740
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A; Residues: 1-111 < RUF>
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Best Local &
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Mus musculus (house mouse)
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Pred. No. 9.4e-36;
0; Mismatches 10
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Pred. No. 1.8e-35;
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23; PMID:1706720
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Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and t
A;Reference number: S40312; WUID:94080891; PMID:8258341
A;Accession: S40367
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A; Experimental source: & C; Superfamily: immunoglo C; Keywords: heterotetran
                                                            A;Accession: A01926
A;Molecule type: protein
A;Residues: 1-108 <SCH>
                                                                                                                                                      A; Title: Determination of the A; Reference number: A01926; MU
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C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change
C;Accession: S40367
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Best Local S
Matches 88
Cross-references: UNIPROT:P01643; Comment: This chain was isolated
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Species: Homo sapiens (man)
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;Status: nucleic acid sequence
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                                                                                             sion: A01240

f, C.; Fougereau, M.

f, C.; Fougereau, M.

Biochem. 59, 525-537, 1975

Biochem. 59, 525-537, 1975

Betermination of the primary structure of a mouse

Determination of the primary structure of a mouse

Determination of the primary structure of a mouse

Processing the primary structure of a mouse

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82.2%; Pred. No. 3.1e-35;
tive 10; Mismatches 9
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Pred. No. 8.6e-35;
6; Mismatches 13
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Ig kappa chain V-I region (Rei) - human C; Species: Homo sapiens (man) C; Date: 24-Apr-1984 #eequence revision C; Accession: A91663; A01873
                              R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen vollstaendige Aminosaeuresequenz des Proteins.
                                                                                              C;Accession: A91663; A01
R;Palm, W.; Hilschmann,
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A;Title: B-cell proliferation initiated by Ia cross-linking A:Reference number: S69900; MUID:92165291; PMID:1537587
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S69900
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F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
A; Reference number: A91663; A; Accession: A91663
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IVM>
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A;Accession: S69907
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78.7%;
                  MUID:76023758;
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Pred. No. 9e-35;
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Pred. No. 9e-35;
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                  PMID:809329
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A;Crose-references: GB.M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1; PID:g196896 A;Note: the authors translated the codon TTC for residue 1 as Leu C;Superfamily: immunog1obulin V region; immunog1obulin homology C;Keywords: heterotetramer; immunog1obulin C;Keywords: heterotetramer; immunog1obulin F;30-104/Domain: immunog1obulin homology <IMM>
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Biochemistry 17 molecular structure of a dimer composed of the variable portions A;Reference number: A90392; MUID:76039968; PMID:1182131
A;Contents: annotation; X-ray crystallography, 2.0 angstroms C;Comment: This is a Bence Jones protein.
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - C;Speciles: Mus musculus (house mouse) C;Date: 14-Feb-1997 #sequence revision 13-Mar-199C;Accession: $69903; $69904; $69905 R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Camb
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A; Residues: 1-108 < PAL>
A; Cross-references: UNIP
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A; Residues: 1-122 < CHE>
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A;Cross-references: GDB:136264
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                                                                                                                                                                                                                                                                                                               DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLIHYTSRLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESGSGSGTDYTETISSLQPEDIATYYCQQYQSLPYTEGQGTKLQITR
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 454; DB 2;
Pred. No. 4.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 456; DB 1;
Pred. No. 2.5e-34;
7; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
  K.R.; Cambier, J.C.
                                            13-Mar-1997 #text_change
                                                                                              mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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Ig kappa chain precursor V region (anti-phenyloxazolone, 18C10) - C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 2
C;Accession: JI0080
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes
A;Reference number: JL0076; MUID:89096973; PMID:3211160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunology 75, 116-121, 1992
A,Title: B-Cell proliferation initiated by Ia cross-linking and sustained by interleukin A,Title: B-Cell proliferation initiated by Ia cross-linking and sustained by interleukin A,Accession: S69903
A,Accession: S69903
A,Status: preliminary; translation not shown
A,Molecule type: DNA
A,Residues: 1-108 <WYS>
A,Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030
                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M27793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A;Note: the authors translated the codon AGG for residue 30 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F;7-115/Product: Ig light chain #status predicted <MAT>
F;22-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-108 <WY2>
A;Cross-references: EMBL:X55045; NID:g511031;
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A;Status: preliminary; translation not shown
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A;Status: preliminary; translation
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A; Residues: 1-115 < KAA>
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                                                                                                                                                                                                                                                                                            F;30-40/Region:
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                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                                                         DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQXPDGTVKLLIYYTSRLHSGVPS
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                                                                                                                                                                                79.6%; Score 452; DB 2;
79.6%; Pred. No. 6.2e-34;
tive 11; Mismatches 11
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RESULT 14 S52789 Ig kappa chain V region

human (fragment)

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RESULT 15
S44118
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <HAW>
A;Residues: 1-110 <HAW>
A;Residues: 1-100 <HAW>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V-J region - human (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001 (;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001 (;Accession: S44118 R;Hawkins, R.S.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994 A;Description: Idiotypic_vaccination against human B-cell lymphoma: rescue of variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mENA
A;Molecule type: mENA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Search completed: December 23, 2004, 19:06:05 Job time: 6.83589 secs
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A; Accession: S52789
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Best Local
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                                                                                                                                                                                                                                                                                                                                   / Match 79.2%; Score 450; DB 2; Length 110; Local Similarity 80.9%; Pred. No. 8.9e-34; res 89; Conservative 6; Mismatches 13; Indels
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87; Conserv
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                                                                                                                                              RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLP--WTFGQGTKVEIKR 108
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                                                                                                        RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPPGVTFGPGTKVDIKR 110
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Match
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568
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1: uniprot_sprot:*
2: uniprot_trembl:*
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  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q91WF8
Q6GMX9
KV5U MOUSE
Q7Z3Y4
Q9JL84
Q6GMX8
AAR11052
KV1H HUMAN
Q6GMX0
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KV1Y_HUMAN
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KV10 HUMAN
AAR10992
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P01608 homo sapien
P01610 homo sapien
Q9ul70 homo sapien
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Q6gmx9 homo sapien
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P01607 homo sapien
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P01596 homo sapien	homo		P01611 homo sapien	Aah34141 homo sapi	Q6pih7 homo sapien	homo	P01606 homo sapien	Q9ul81 homo sapien	homo	homo	pollo	P01609 homo gapien

# ALIGNMENTS

Minimum DB Maximum DB

Searched:

Scoring table: Sequence:

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				ALIGNMENTS	K. N. I. W.
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( )	Eukaryota;		Chordata;	Craniat	Craniata; Vertebrata; Euteleostomi;
. ( )	Mammalia; Eutheria;		Primates;	Catarrh	ini; Hominidae; Homo.
4 7	NCBI_TaxID=	9606;			
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	Hoppe-Seyler's	87	Physiol. Chem.		353:345-370(1972).
ъ.	X-RAY CRYSTALLOGRAPHY.	ALLOGRAPH'	Υ.		
, ,	MEDLINE=77022433; PubMed=1234024;	22433; Pu	bMed=1234		7
	Schwager P.	. Steigem	ann W., S		H.J.:
Τ,	"The structure determination of the	ure deter	mination (		variable portion of the Bence-
3		protein Au.";		146/1075	
( ) [	-1- MISCELL	MISCELLANEOUS: The	he struct	structure of the	V region was determined
1 ( 1	molecular	ar replac	replacement methods using	hods usi	the known st
( ) (	ī	LANEOUS: T	he C regio	on of this	is chain has the INV (3) marker.
()	-!- MISCELL	~	his is a l	Bence-Jones	protein.
0 20	PIR; A91653;	KIHUAU.	1-107		
, 0		576; C:exi	tracellul	ar; NAS.	
טג נ		GO:0003823; F:antigen binding; NA	tigen bin	ding; NAS	. ·
,U ,	InterPro; I	PR007110;	Iq-like.	OHRE; NAS	o.
, 20	InterPro; I	IPR003596; Ig_v.	Ig_v.		
	SMART: SMOD4O6: TGV:	406. IGV:	_		
, 0,	PROSITE; PS50835; IG	50835; IG	LIKE; 1.		
t, 2,	3D-structure;	₽en		protein; Di	Direct protein sequencing;
	DOMAIN	۲,	:	Framework-1.	k-1. ·
7 -3	DOMAIN			Compleme:	Complementarity-determining-1.
-, -	DOMAIN			Complementa	Complementarity-determining-2.
-	DOMAIN	57	88 1	Framework-3.	x-3.
, -,	DOMAIN			Compleme	Complementarity-determining-3.
7	DISHLETD			Pramework-4.	K-4.
-3'	STRAND		ຫ່		

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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RC STRAIN=FVB/N; TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Alausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., MAX S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., MAX S.I., Wang J., Hosg L.,

RA Hopkins R.F., Jordan H., Moore T., MAX S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bahs S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., W., Green E.J., Lu X., Gibbs R.A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RT "Generation and initial analysis of more than 15,000 full-length human

"Ten and mounes c.DNA secmenes":
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein (Fragment).
Mus musculus (Mouse).
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                                                        mouse cDNA sequences.";
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                                         Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11939 MW;
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                                         U.S.A.
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                         99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E8011187EE6F6FB9 CRC64;
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RESULT 3

KV5J_MOUSE

ID KV5J_MOUSE

AC P01643;

DT 21-JUL-1986

OS MUSELITAXID-1

RN [1] TAXID-1

RN [1] TAXID-1

RN MEDLINE=760

RN MEDLINE=760

RA SCAIFF C., I

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DR PIR, A01926,

RT PIR, A01
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.26; KVMS73.
.26; KVMS73.
.201594; IJV5.
InterPro; IPR0070110; I5
InterPro; IPR003596; Ig_\
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
23 Comple.
101 24 Comple.
102 Comple.
103 49 Framewon
104 57 88 Framewon
105 66 Complement
106 108 108
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Best Local Similarity
Matches 86; Conserv
Query Match
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Interpro; IPR003597; Ig.cl.
Interpro; IPR003597; Ig.cl.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PP00654; Cl.set; I.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           "Determination of the primary structure of immunoglobulin. Amino-acid sequence of the Eur. J. Biochem. 59:525-337(1975).

-I- MISCELLANEOUS: This chain was isolated PIR; A01926; KVMS73.

HSSP; P01594; 1JV5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01643;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence
05-JUL-2004 (Rel. 44, Last annotati
19 kappa chain V-V region MOPC 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC013496; AAH13496.1; -. PIR; A38740; A38740. PIR; C38740; E38740. PIR; E38740; E38740. PIR; B38740; G38740.
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PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=76091934; PubMed=812696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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81.2%;
                                            MW;
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annotation updat
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                                                                                                                                                                                                                                                                                   Immunoglobulin V region
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Pred. No. 9.2e-
12; Mismatches
Score 461;
                                                                                                                 Framework-3.
Complementarity-determining-3.
Framework-4.
                                                                                                                                                                                        Complementarity-determining-2
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                                                                                           By similarity.
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                                            2AD29D92A72AA0A3 CRC64;
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DB 1;
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light chain.";
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Length 108;
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RC STRAINE-FYB/N, TISSUS-Colon,

RC STRAINE-YB/N, Schuler G.D.,

RC SCHULER G.D., Schemen C.M., Schuler G.D.,

RC ALL SCHULER G.D., MART S.D., Male N.A., Rubin G.M., Hong L.,

RC SCHULER G.D., MC SCHULE G.D., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA RILL RC SCHULE S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA RILL RC SCHULE S., Garcia A.M., Rodrigues S., Sanchez A.,

Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA RODRIGUEZ A.C., GRANG R.B., Schmutz J., Myers R.M., Schein J.E.,

RA RODRIGUEZ A.C
                                                                                             Query Match
Best Local Similarity
Matches 86; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-Bet; I.
Pfam; PF00767; Ig; 1.
SMART; SM00406; IGy; 1.
SMART; SM00406; IGy; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50835; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                Hypothetical
SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EC027418; AAH27418.1; P01594; 1JV5.
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DIQMTQSPSSLSASVGDRVTITCSASQDISNYLMMYQQKPDKAVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                al protein.
234 AA; 25858 MW;
                                                                                          81.2%;
illarity 79.6%;
Conservative 1:
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                                                                                          Score 461; DB Pred. No. 2.4e
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3; Mismatches
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                                                                                                                                                                                                                4EB08C81426AEAB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
annotation update)
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ches 10;
                                                                                                                      DB 2;
.4e-40;
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PDB; 1AR2; X-ray; @=1-107.
PDB; 1BWW; X-ray; A/B=1-107.
PDB; 1REI; X-ray; A/B=1-107.
PDB; 1REI; X-ray; A/B=1-107.
GO; GO:00005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Epp O., Lattman E.E., Schiffer M., Huber
"The molecular structure of a dimer compo
                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Palm W., Hilschmann
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986
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"The primary structure of a crystalline monoclonal immunoglobulin
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      Bence-Jones
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Ig kappa chain V-V region HP R1
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI TaxID=10090;
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STRAIN=B6.Sle1; TISSUE=Spleen;
STRAIN=B6.Sle1; TISSUE=Spleen;
Liang Z., Xie C., Chen C., Kreska D., Hsu K., 7

"Antinuclear autoantibodies from B6.Sle1 mice.
"Antinuclear autoantibodies from B6.Sle1 mice.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ

""" AY436832; AAR10992.1; -.
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                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-V region HP R16.7.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment).
Mus musculus (Mouse).
Mus musculus (Mouse).

Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae;
                                                                                                                                                                                                                                                                                                   P01644;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                           KV5K_MOUSE
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111 AA;
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Pred. No. 5.
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Pred. No. 3.
                                                                        Craniata; Vertebrata; |
Sciurognathi; Muridae;
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DE 19 kappa chai

OS Mus musculus

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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1

Direct protein sequencing; I

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Mammalia; Eutheria;
NCBI_TaxID=10090;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Direct protein sequencing;
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HSSP; P01594; 1JV5.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                     "Complete amino acid sequence of light chain vari
from five monoclonal anti-p-azophenylarsonate ant
with respect to a crossreactive idiotype.",
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981)
                                                                                                                                                                                        Siegelman M., Capra
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STRAIN=A/J;
                                                                                                                         -!- MISCELLANEOUS: Anti-arsonate
                                                                                                                                                                                                   MEDLINE=82150934; PubMed=6801658;
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Rodentia;
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Pred. No. 3
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Complementarity-determining-3.
Framework-4.
By similarity.
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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21-JUL-1986
05-JUL-2004
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive didotype.", Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003596; Ig_v.
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                    RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR
                                                                                          DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS
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RFSGSGSGTDYSLTISNLEQEDIATYFCQQGYMLPRTFGGGTKLEIKR
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01, Last sequence up
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; Pred. No. 2.9e-
8; Mismatches
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Pred. No. 2.9e
10; Mismatches
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Framework-3.
Complementarity-determining-3.
Framework-4.
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                                                                     SNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
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2.9e-39;
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Best Local S
Matches 85
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HSSP; P01607; 1BWA.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                P01648;
21-JUL-1986
21-JUL-1986
05-JUL-2004
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NON TER
SEQUENCE
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Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones prote: complete sequence and the location of the disulfide bridge: J. Biol. Chem. 244:3550-3560(1969).
-!- MISCELLANEOUS: The C region of this chain has the INV
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 SEQUENCE.
STRAIN=A/J;
                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                            Mus musculus (Mouse)
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DOMAIN
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Bence-Jones protein; Direct
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Mammalia; Eutheria; Primates;
                                         NCBI_TaxID=10090;
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                                                                                                                                    kappa chain
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(Rel. 01, Last sequence update)
(Rel. 44, Last annotation updat
in V-V region HP 91A3.
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                                                                             Chordata;
Rodentia;
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78.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 445; DB 1;
Pred. No. 4.7e-39;
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Complementarity-determining-2
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Complementarity-determining-1.
                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 12
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Best Local 9
  Query Match
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PIR; S34083; S34083.

HSSP; P01607; 1BWW.

InterPro; IPR007110; Ig-like.

IntexPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 1

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.
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"Complete
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DOMAIN
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MEDLINE=98277139; PubMed=9614934;
WW.X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. EMBL; AF035037; AAD56273.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL77;
01-MAY-2000
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PROSITE; PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- MISCELLANEOUS: Anti-arsonate hybridoma protein. HSSP; P01594; 1475.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                          Young
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                                                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies
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77.8%;
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Ig_v.
                                       11738 MW;
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  78.3%;
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Last annotation update)
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  Score 445;
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Pred. No. 4.7e-39;
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By similarit
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                                         C06681716C4D16F3
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Length 108;
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Matches 86; Conserv
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Best Local Similarity
Matches 85; Conserv
        Q6GMW1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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21-JUL-1986
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SEQUENCE
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                    Q6GMW1
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Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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21-JUL-1986 (Rel. 01, Last
05-JUL-2004 (Rel. 44, Last
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el. 44, Last annotation
V-V region HP 124E1.
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Pred. No. 7.7e
10; Mismatches
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7; Mismatches
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Complementarity-determining-3
Framework-4.
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         sequence update) annotation updat
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No. 7.7e-39;
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RESULT 15

KVIP HUWAN STANDARD; PRT; 108

ID KVIP HUWAN STANDARD; PRT; 108

AC P01608;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence upda

DT 05-JUL-2004 (Rel. 44, Last annotation up

DE 1g kappa chain V-I region Roy.

OS Homo sapiens (Human).

OC Bukaryote, Metazoa; Chordata; Craniata;

OC Mammalia; Eutheria; Primates; Catarrhini
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Best Local S
Matches 87
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

A Listchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Listchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M., Ugdin T.B., Bonaldo M.F., Carninci P., Prange C.,

A Brownstein M., Ugdin T.B., Bonaldo M.F., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny B., Wetteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003599; IG-
InterPro; IPR003597; Ig-C1.
InterPro; IPR003597; Ig-C1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00654; C1-Bet; T.
Pfam; PP00047; Ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC; 1.
SMART; SM00407; IGC; 1.
SMART; SM00407; IGC; 1.
SMART; SM00406; IG, 1.
SMART; SM00407; IGC; 1.
SMART; SM00406; IG, 1.
SMART; SM00406; I
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Submitted (JUN-2004) to the
EMBL; BC073791; AAH73791.1;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Proc. Natl. Acad. Sci. U.S.A.
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Framework-4.
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# SUMMARIES

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	Abr42287	Abr42288	Abr42291	Abr42290	Abr42293	Abr42295	Aar79866	Aar79887	Aao18391	Aau72801	Adj79787	Aao29869	Aab20434	Adj79825	Aao29882	Aau72814	Aab20435	Adf72734	Adf72729	Adf72730
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AAB81989 standard; protein; 119 AA

AAB81989;

03-JUL-2001 (first entry)

Ganglioside GD3 specific antibody related protein SEQ ID NO:

Ganglioside; GD3; complementarity determining region; CDR; antibody; cancer.

Mus musculus.

WO200123432-A1.

05-APR-2001.

29-SEP-2000; 2000WO-JP006774

30-SEP-1999; 99JP-00278291. 06-APR-2000; 2000JP-00105088.

(KYOW ) KYOWA HAKKO KOGYO KK.

Hanai N, Shitara K, Nakamura ζ, Niwa Ø

WPI; 2001-266143/27.

New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent

activity in cancer.

Claim 10; Page 173-174; 183pp; Japanese.

The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

Sequence 119 AA;

Query Match 100.0%; Score 624; DB 4; I Best Local Similarity 100.0%; Pred. No. 7.4e-51; Matches 119; Conservative 0; Mismatches 0; Length 119; Indels 0, Gaps 0

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     AAR33256;
                                                      AAR33256 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 112-113; 121pp; Japanese.
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                                                      protein; 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 624; DB 6;
Pred. No. 7.4e-51;
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RESULT 4
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Best Local
         Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR33256-57 represent rat heavy and light chain variable regions respectively. The DNA sequences encoding these proteins were used in the construction of humanised chimeric antibody expression vectors. In these humanised antibodies none of the amino acids of the non-human animal Ab variable region have been changed. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Promoter; v
humanised;
                                                                                                                               AAR53341 standard;
                                                                                                                                                                                                                                                                                                                                   Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised chimeric antibody prodn. against ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ33257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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12-JUL-1993
                                                          KM641 L
                                                                                 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-095510/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-1991;
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                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 29-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as melanoma,
                                                                                                                                                                                         SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS
                                                                                                                                                                                                                                        EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variable; region; rat; immunoglobulin; heavy;
; chimeric; antibody; expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanai N,
                                                                                                                                                                                                                                                                                      Conservative
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(first entry)
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAKKO
                                                        variable region.
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11. .130
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                                                                                                                             protein; 130
                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroblastoma,
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                                                                                                                                                                                                                                                                                    Score 624; DB 2;
Pred. No. 8.2e-51;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide"
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RESULT 5
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XX AAY2
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XX PMM6
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2 describes the construction of the vector pChi641HA1 for chimeric human antibody H chain expression. mRNA from mouse anti-GD3 monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain cDNAs isolated. The base sequences of the Ig variable regions in KM641 H chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector was constructed by joining the H chain variable region gene from pKM641HA3 to a vector for chimeric human Ab H chain expression using the synthetic DNAs given in AAQ63439 and AAQ63440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised cytocidal
  07-SEP-1993;
                                                                                                                                                                                                                                                                                                                            pKM641 HA3 immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28369
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                                                  07-JUN-1995;
                                                                                                    17-AUG-1999
                                                                                                                                                   US5939532-A
                                                                                                                                                                                                   Muв вр.
                                                                                                                                                                                                                                                     antibody; nucleotide; genomic; hypervariable region; chimeric;
light chain; amino acid.
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody specific for ganglioside GM2 - used for producing a effect on cancers such as melanoma, neuroblastoma and glioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 116-117; 191pp; English
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  93US-00116778
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Pred. No. 8.2e-51;
Mismatches 0;
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RESULT 6
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ID AAB0
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Matches 119
WPI; 2000-402204/35.
N-PSDB; AAA51003.
                                                                                                                                                                           18-SEP-1991;
18-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine immunoglobulin heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no methionine initiation codon and the leader sequence was partly lacking. The chimeric human antibodies are useful in the treatment of cancer, especially that which is of neural ectodermal origin. In contrast to prior art constructs based on mouse monoclonal antibodies, the chimeric human antibodies do not cause anti-mouse immunoglobulin production. The chimeric human antibodies human antibodies have a prolonged half-life and
                                                                                                                                                                                                                                                                                                     28-JUN-2000
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a reduced frequency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Col 99-101; 188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin; H chain; heavy chain; variable region; cancer;
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                                                                                                                         куома накко кодуо
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                                                                        Hanai N,
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                                                                                                                                                                        91JP-00238375.
92EP-00116026.
                                                                                                                                                                                                                                                   99EP-00124345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          /label= mature_immunoglobulin_heavy_chain_variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of adverse effects when compared to mouse monoclonal
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100.0%; Pred. No. 8.2e-51;
                                                                        Hasegawa
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   The present invention describes a monoclonal antibody which can reac specifically with ganglioside GD3. The antibody and its derivatives useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplifica of the invention
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                                                                                                                                                                                                                                                             New human type complementation-determining region-transplanted and derivatives against ganglioside GD3, useful in diagnosis ar of e.g. tumors, with low antigenicity, little side effects but
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06-APR-2000; 2000JP-00105088.
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                                                                                                                                                                           Example 1; Page 138-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Shitara K,
                                                                                                                                                                                                                                        cancer.
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Pred. No. 8.2e-51;
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Best Local S
Matches 119
                                                                                                                                                                                                       Query Match
Best Local S
Matches 119
                                                                                                                                                                                                                                                                                                                                                    The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumo like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reactions, particularly to relieve problems of side-effects during the conventional single administration. This seque represents a protein associated with the anti- ganglioside GD3 antibod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drugs containing genetically-modified antibody against ganglioside GD: its fragment, immunocompetent cell activators or/and antitumor agents combination, applicable in treating malignant tumor like melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                            Sequence 138
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                             SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                  EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
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  SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS
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                                                                                                                                                                                                          Conservative
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Pred. No. 8.7e-51
                                                                                                                                                                                                       Score 624; DB 6;
Pred. No. 8.7e-51;
Mismatches 0;
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RESULT 9
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XX O5-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1999; 99JP-00278291
06-APR-2000; 2000JP-00105088
Synthetic
                                     Ganglioside;
                                                               Ganglioside
                                                                                          03-JUL-2001
                                                                                                                                           AAB81985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 39; Page 175-179; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanai N,
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                                                                                                                                                                                                                                                                                                                                                                                              the invention
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119; Conserv
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                                                                                                                                                                                                                                                                                                                 Conservative
                                       GD3;
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                                                                                         (first
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                                                              specific antibody related
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                                       complementarity
                                                                                                                                          protein; 119
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                                                                                         entry.
                                                                                                                                                                                                                                                                                                              100.0%; Score 624; DB 4;
100.0%; Pred. No. 4.2e-50;
tive 0; Mismatches 0;
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                                       CDR; antibody;
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RESULT 11
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Best Local Sim
Matches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
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                    WPI; 2003-067410/06
                                         Shitara
                                                                                                           29-MAR-2002; 2002WO-JP003170
                                                                                                                                  10-OCT-2002.
                                                                                                                                                                            Synthetic
                                                                                                                                                                                                 Ganglioside
                                                                                                                                                                                                                                             04-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 119
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                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                     29-MAR-2001; 2001JP-00097483
                                                                                                                                                      WO200278739-A1
                                                                                                                                                                                                                      Modified ganglioside GD3 antibody associated protein
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06-APR-2000; 2000JP-00105088.
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                                       Niwa R,
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Pred. No. 1.2e-46;
5; Mismatches 5
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Drugs containing genetically-modified antibody against ganglioside GD3

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RESULT 12
AAB81987
ID AAB81
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Best Local :
The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reactions, particularly to relieve problems of side-effects during the conventional single administration. This sequence represents a protein associated with the anti- ganglioside GD3 antibody
                                                                                                                                                                                                      New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ganglioside;
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                                                                                                                                     Claim 41; Page 168-172; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                            WPI; 2001-266143/27.
                                                                                                                                                                                                                                                                                                                                                     Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-1999; 99JP-00278291.
06-APR-2000; 2000JP-00105088.
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91.6%;
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Pred. No. 1.2e
5; Mismatches
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.2e-46;
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                        exemplification
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Sequence 582 AA;

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Best Local S
Matches 109
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                                                                                                                                                      the usual hybridoma techniques. The coding sequence for the variably region can be used to generate humanised variants, especially by mutagenic PCR. CD6 has been shown to be expressed in T lymphocytes involved in the inflammatory infiltration of the skin in psoriasis. anti-CD6 MAb can therefore be used to diagnose and treat psoriasis. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                This is the amino acid sequence of the heavy chain variable region of the monoclonal antibody (MAb) ior TIA which recognises the human leukocyte differentiation antigen CD6. The MAb is a murine IgG2-type Ab produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR;
                                                                                                                              Sequence 119
                                                                                                                                                                                                                                                                                    Claim 3; Page 27; 38pp; Spanish
                                                                                                                                                                                                                                                                                                              Monoclonal antibody against human CD6 antigen - useful for diagnosis treatment of psoriasis.
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12-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                          Montero Casimiro
                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1995;
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                                                                                        Local
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SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                          EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPEKRLEWVATISSGGSYIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in; variable region; monoclonal antibody; human; CD6; murine;
differentiation antigen; hybridoma; humanisation; mutagenesis;
er; amplification; inflammatory infiltration; skin; psoriasis;
                                                                            Conservative
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Pred. No. 7e-46;
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Pred. No. 1.5e-38;
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Query Match
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Score 487;

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Sequence 134 AA;

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RESULT 14
ABP60555
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                                      The invention relates to a novel monoclonal antibody having the identifying characteristics of, or that is a monoclonal antibody 14F3. An antibody of the invention has osteopathic, antirheumatic, antiarthritic, antiinflammatory, cyrostatic, antipsoriatic, antidiabetic, and neuroprotective activity. The polynucleotides encoding the antibodies of the invention may have a use in gene therapy. The antibodies and polypeptides are useful for treating or preventing osteopathic diseases, such as rheumatoid architis, osteoporosis, metastatic and primary bone cancer, wear debris induced osteolysis or osteoarthritis, and immune diseases such as psoriasis, insulin-dependent diabetes, inflammatory bowel disease or multiple sclerosis. The present sequence represents the heavy chain variable region of the murine monoclonal antibody 14F3 of the invention. The sequence contains three complementary determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic; antiarthritic; antinflammatory; cytostatic; antipsoriatic; antidiabetic; neuroprotective; gene therapy; rheumatoid arthritis; osteoporosis; bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis; insulin-dependent diabetes; inflammatory bowel disease; multiple sclerosis; heavy chain variable region;
                                                                                                                                                                                                                                                                                                     New monoclonal antibody having the characteristics of a monoclonal antibody 14F3, useful for treating or preventing osteopathic diseases, e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.
                                                                                                                                                                                                                                                          Disclosure; Page
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                                                                                                                                                                                                                                                                                                                                                                       ABV99887.
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99. .110
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50. .66
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RESULT 15
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Peptide
                       Scheiflinger F,
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                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                         Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
                                                         14-SEP-1999;
                                                                         13-SEP-2000; 2000WO-EP008936
                                                                                                         WO200119992-A2
                                                                                                                                                                   Protein
                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                         Anti-FIX/FIXa antibody 198/B1-myc-tag fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB20442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20442 standard; protein;
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                                        BAXTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARLDGYNYRWYPDVWGTGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLVESGGDLVKPGGSLKLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                         99AT-00001576
                       Kerschbaumer
                                                                                                                        /label= His_tag
                                                                                                                                          'label=
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                              label= VH
                                                                                                                                                         label= Myc_tag
                                                                                                                                                                           label= Spacer
                                                                                                                                                                                                            label=
                                                                                                                                                                                                                             note= "encoded
                                                                                                                                                                                                                                                             label= scFv
                                                                                                                                                                                                                                                                               label= Mature_protein
                                                                                                                                                                                                                                                                                              label= Signal_peptide
                                                                                                                                                                                            label= VL
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                                                                                                                                                                                                             Linker
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6; Mismatches
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                       Falkner F,
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                       Dorner F,
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                                                                                                                                                                                                                                                                                                                                                                         myc-tag
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Search completed: December 23, 2004, 18:57:39 Job time: 33.8339 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a fusion protein comprising: a PelB CC leader; a single chain FV (scFV) derivative of antibody 198/B1 comprising CC the heavy (VH) and 11ght (VL) chain variable regions of 198/B1 comprising CC an artificial, flexible linker paptide; a spacer; a Myc-tag peptide; a CC spacer; and a C-terminal GHIs affinity tail 198/B1 is an example of anti-cc chaman Factor IX (FIX)/activated Factor IX (FIXA) antibodies of the CC invention. Anti-FIX/FIX antibodies and their derivatives, including scFv CC fragments, have FVIIIa cofactor activity or FIXA activating activity. CC Administration leads to an increase in the procoagulant activity of FIXA, CC even in the presence of FVIIIA inhibitors. This allows for rapid blood CC coagulation even in the absence of FVIII or FVIIIA, and in the case of CC FVIII inhibitor patients. The antibodies and derivatives are used in a CC claimed pharmaceutical composition for treating patients with blood CC coagulation disorders, especially haemophilia A and haemorrhagic CC diathesis. The scrivity crag fusion was expressed in E. coli. It exhibited CC FVIII-like activity.
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Best Local S
Matches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 294 AA;
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FVIII-like activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 18; Fig 34; 138pp; English.
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Local Similarity 78.7%;
hes 96; Conservative
                                                                                                                                                143
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                                                                                                                                                                                                                                                                                  83 PDSVKGRFTISKDNAKNTLYLQMSSLASEDTAMYYCTREGGGFTVNWYFDVWGAGTSVTV 142
                                                                                                                                                                                                                                                                                                                              61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLG---TYYFDSWGQGTTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                           SS 144
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Post-processing: Minimum Match 0%
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
        BG
  US-09-225-322B-18
US-09-7264-304-18
US-09-725-322B-18
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US-09-764-304-8
US-09-764-304-8
US-08-875-674A-3
US-08-875-674A-3
US-08-875-378A-16
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US-08-484-508-16
US-08-356-378A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
Sequence 18, Appl Sequence 8, Appli Sequence 8, Appli Sequence 2, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appli Sequence 11, Appli Sequence 20, Appli Sequence 4, Appli Sequence 16, Appli Sequence 2, Appli Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304
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Query M Best Lo Matches Qy Db Db	CURREN PRIOR	RESULT 1 US-09-225- ; Sequence ; Patent N GENERAL ; APPLICA	22 22 23 23 23 24 24 24 25 26 26 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28
Match OO.0%; Score 624; DB 4; Le Occal Similarity 100.0%; Pred. No. 8.8e-66; 19; Conservative 0; Mismatches 0; I  1 EVTLVESGGDEVKPGGSLKVSCAASGFAFSHYAMSWVRQTPA	NT APPLICATION NUMBER: 199-APPLICATION NUMBER: 199-APPLICATION NUMBER: 1995-05-APPLICATION NUMBER: 1995-05-APPLICATION NUMBER: 1911-101-101-101-101-101-101-101-101-101	ALIGNMENTS  322B-18 18. Application US/09225322B 10. 6437098 1INFORMATION: ANT: SHITARA, KENYA ANT: HANAI, NOBUO ANT: HASEGAWA, MAMORU ANT: HASEGAWA, MAMORU ANT: MIYAJI, HIROMASA ANT: KUWANA, YOSHIHISA ANT: KUWANA, YOSHIHISA ANT: KUWANA, YOSHIHISA ANT: KUWANA, YOSHIHISA	448.5 71.9 443 5 PCT-US96-13152-4 447 71.6 119 1 US-08-331-398A-46 447 71.6 119 2 US-08-331-397B-46 447 71.6 119 2 US-08-759-804A-46 447 71.6 119 3 US-09-227-93-46 447 71.6 119 3 US-09-227-93-4 447 71.6 123 3 US-09-344-587-13 445 71.3 117 3 US-08-752-93A-3 445 71.3 117 3 US-08-752-93A-3 445 71.3 136 3 US-08-976-183A-31 445 71.3 136 3 US-08-976-183A-32 445 71.3 136 3 US-08-976-183A-34 445 71.3 245 4 US-09-956-086-5 445 71.3 245 4 US-09-956-087-5 445 71.3 245 4 US-09-956-087-5 445 71.3 246 5 4555030-9 444.5 71.2 247 6 5455030-9 444.7 71.2 125 2 US-08-428-197-1
Length 130;  Indels 0; Gaps 0;  PAKRLEWVAYISSGGSGTYY 60		CHIMERA ANTIBODY	Sequence 4, Appli Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 13, Appl Sequence 31, Appl Sequence 31, Appl Sequence 32, Appl Sequence 32, Appl Sequence 33, Appl Sequence 34, Appl Sequence 5, Appli Sequence 5, Appli

Patent No. 6495666

INFORMATION:

APPLICANT: SHITARA, APPLICANT: HANAI, N

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APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MUYANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US 08/292,178
                                       GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, VOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT FILING DATE: 199-01-05
CURRENT FILING DATE: 199-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-11
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/22,178
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1991-09-18
NUMBER OF SEO ID NOS: 19
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Best Local S
Matches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09225322B Patent No. 6437098 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
                          NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1991-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 EVTLVESGGDEVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 SDSVKGRFTISRDNAKNTLYLOMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS
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PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 624; DB 4; Length 130; nilarity 100.0%; Pred. No. 8.8e-60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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US-08-875-674A-1 US-08-875-674A-1 ; Sequence 1, Application US/08875674A ; Patent No. 6572857

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TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER APPLICATION NUMBER: US07/947,674
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, FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8
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US-09-764-304-8
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                                                                                                                                                                                                                                                                 US-09-764-304-8
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                          Query Match 98.4
Best Local Similarity 99.2
Matches 118, Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHITARA, APPLICANT: HANAI, N
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: CDNA KM-641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 130
71
                          61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
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                                                                                  EVTLVESGGDFVKÞGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAGISSGGSGTYY
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    SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS
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99.2%;
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Pred. No. 1.1e-58;
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Pred. No. 1.1e-58;
                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                       DB 4; Length 130;
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RESULT 6
PCT-US94-07659-2
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Patent No. 6572857
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 Amino acid
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OPERATING SYSTEM: Windows 95.
SOFTWARE: Word Perfect 5.0 for Windows 95.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,674A
FILING DATE: 17-Jully-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/CU96/00004
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Unc CITY: Scarsdale CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: P.
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: -N Terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk 3.5' (1.4 MB).

COMPUTER: Compatible PC IBM (80486, 8 M Ram).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 119 Amino acid residues.
TYPE: Amino acid.
STRANDEDNESS: Unknown.
TOPOLOGY: Unknown.
                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mice Balb/C INDIVIDUAL ISOLATE: ic TISSUE TYPE: Murine h:
                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD: Experimental.
OTHER INFORMATION: Sequence corresponding to the variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                 61 SDSVKGRFTISRDNAKNTLYLØMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                     97;
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                                                                             PDSVKGRFTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLDYFDSWGQGTTLTVSS 119
                                                                                                                                                        EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPEKRLEWVATISSGGSYIYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sub-clone ior t1A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (914)-723-4301
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MONTERO CASIMIRO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (914) 723-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLATE: ior tlA
Murine hibridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                    79.0%;
                                                                                                                                                                                                                                                                                                                               of the heavy chain of the monoclonal antibody recognizing hur designated as sub-clone for tlA.
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Pred. No. 1e-45;
3; Mismatches
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                                                                             Sequence 3, Application US/08875674A Patent No. 6572857
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.9%;
Best Local Similarity 79.0%;
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                                    GENERAL INFORMATION:
APPLICANT: MONTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (610) 270-508
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028 REFERENCE/DOCKET NUMBER: P50 TELECOMMUNICATION: (610) 270-5024
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
PILING DATE: 09-UTL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corporation - Corp ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                80
                                                                                                                                                                                                                         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                                                                                                          94;
                                                                                                                                                                                                                                                                              20 EVHLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTPEKRLDWVAYISSGGGGTYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 amino acids
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Jonak, Zdenka L.
Theisen, Timothy
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Hurle, Mark
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                      LOMBARDERO
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                                         MONTERO CASIMIRO, J. E.
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                    VALLADARES,
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Pred. No. 1.4e-44;
7; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Length 247;
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

P REZ RODR GUEZ, F SIERRA BL ZQUEZ, F TORMO BRAVO, B. R.

Anti-CD6 monoclonal antibodies and their uses

BLASCO,

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RESULT 8
US-08-553-497A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: By similarity with known sequence.
OTHER INFORMATION: Sequence corresponding to the humanized
Patent No. 6572857
OTHER INFORMATION: variant of sub-clone ior tlA recognizing human CD6, particula
OTHER INFORMATION: to the variable region of its heavy chain.
                                                                                                                                                  Patent No.
                                                                                                                                                                    Sequence 18, Application US/08553497A
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/875,674A
FILING DATE: 17-July-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/CU96/00004
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (914)-723-4301
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
FRAGMENT TYPE: -N Terminal fragment.
ORIGINAL SOURCE:
TISSUE TYPE: Animal cells.
CELL LINE: NSO " SP 2/0 " CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Uni
MOLECULE TYPE:
HYPOTHETICAL:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: CITY: Scarsdale CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 5.0 for Windows 95. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk 3.5'' (1.4 MB).

COMPUTER: Compatible PC IBM (80486, 8 M Ram).
                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Compatible read OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 119 Amino acid residues.
TYPE: Amino acid.
STRANDENESS: Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan,
                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                   61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
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10583
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                                                                                                                                                                                                                                                                                                                                                                             1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                    5844093
                                                                                                                                                                                                                                                                PDSVKGRFTISRDNVKNTLYLOMSSLRSEDTAMYYCARRDYDLDYFDSWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                        EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQAPGKRLEWVATISSGGSYIYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sub-clone ior tlA
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
MITJANS, FRANSESC
ROSELL, ELISABET
                                                ANSELL, KEITH F
                                                                                      KETTLEBOROUGH, C. BENDIG, MARY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
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                                   JAUME
                                                                          KEITH H.
                                                                                                                                                                                                                                                                                                                                                                                                                                  76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 480; DB 4; Length 119, Pred. No. 2.6e-44; 4; Mismatches 21; Indels
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US-08-553-497A-18
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                                                                                                                                                                             Sequence 16, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Veri

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,497A

FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT
APPLICATION UNMBER: HO PCT
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 941
PILING DATE: 17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                     APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized :
TITLE OF INVENTION: L-Selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 9.
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN,
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PIULATS, TITLE OF INVENTION:
                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 75.6%;
Local Similarity 77.3%;
nes 92; Conservative
CITY: San Francisco
STATE: California
                ANDDRESSEE: Townson, Ambret Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                                                                           61
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                                       Townsend and Townsend and Crew
we MarketPlaza, Steuart Tower, Suite 2000
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3, JAUME
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ANTIBODIES
                                                                                                                                          Humanized Antibodies Reactive with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO PCT/EP95/00978
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Pred. No. 4.4e-43;
8; Mismatches 19; Indels
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RESULT 10
US-08-326-362-2
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application Patent No. 5730981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95112895.8

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95114696.8

FILING DATE: 19-SEP-1995

ATTONNEY/AGRATION:

NAME: Liebescheutz, Joe O.

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-002220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION UMBER: US/08/579,378A
                                   ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  COUNTRY: USA
                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 27-DEC-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVKLVESGGGLVKPGGSLKLACAASGFTFSTYAMSWVRQTPEKRLEWVASISTGGS-TYY
                                                                                                                       D.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.2%;
79.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 469.5; DB 3;
Pred. No. 4.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 135;
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; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-406-535-2
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US-09-406-535-2
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Connie L. Brickson-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: James D. Winkler
TITLE OF INVENTION: Tie2 Antagonist Antibodies
FILE REFERENCE: P50844
CURRENT APPLICATION NUMBER: US/09/406,535
CURRENT APPLICATION NUMBER: 60/102,100
EARLIER APPLICATION NUMBER: 60/102,100
EARLIER FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
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Best Local Similarity
                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 08 795.3
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Einaudi, Carol P. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
61 ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAIYYCARGYYGPYYFDYWGQGTALTVSS 119
                      61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARGG-SRYAMDYWGQGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
                                                                                                                                                                    Similarity
                                                                        EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSSTITY 60
                                                                                                      EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                  74.4%;
ilarity 74.8%;
Conservative
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                                                                                                                                                  Score 464; DB 3; Length 119; Pred. No. 1.4e-42; B; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 466.5; DB 1
Pred. No. 7.3e-43;
7; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 118;
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US-09-518-737-2

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APPLICANT: RUDERT, FRITZ
APPLICANT: GE, LIMING
APPLICANT: GE, LIMING
APPLICANT: GE, LIMING
TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
TITLE OF INVENTION: (POLY) PEPTIDE COMPLEX
FILE REFERENCE: MORPHO)9
CURRENT PILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: US/09/495,880A
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: ECT/EP98/04836
PRIOR APPLICATION NUMBER: ED 97 11 3319.4
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-2
                                                                                         US-09-495-880A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-495-880A-11
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APPLICANT: FUKUI, YASUHISA
APPLICANT: NAGATA, SATOSHI
APPLICANT: SHIRAL, RYUICHI
APPLICANT: SHIRAL, RYUICHI
APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
FILE REFERENCE: 1965/49618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
Query Match 73.3%;
Best Local Similarity 75.8%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6667150 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09495880A
Patent No. 6667150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09518737 Patent No. 6709833
                                                                                                                                                                                                                                      SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 92;
                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv
OTHER INFORMATION: HAG)-gene IIIss encoded by phage vector fhaglA (cir
                                                                                                                                                                                              LENGTH: 456
TYPE: PRT
                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARQRGYVNFGIAY---WGQGTLVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVESGGDLVKPGGSVKLSCAASGFTFSSYGMSWARQTPDKRLEWVASISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 3.4e-42;
Pred. No. 3.7e-42;
Score 457.5; DB
Pred. No. 3.6e-41
B; Mismatches 2
                                        DB 4;
    20;
                                        Length 456;
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  Indels
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Gaps
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(circular)
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FILE REFERENCE: p1775R1
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
LENGTH: 119
TYPE: PRT
                                                     ; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH consens
US-09-648-067A-15
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PCT-US94-14106-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein PCT-US94-14106-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.6
Conservative
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09648067A Patent No. 6627196
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies FILE REFERENCE: P1775R1
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baughman, St
APPLICANT: Shak Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDSAMYYCARRERYDENGFAYWGQGTLVTVSA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNAKNNLYLOMNSLKSEDTAMYYCARDPL----YGSWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVKLMESGGDLVKPGGSLKLSCAASGFTFSDYYMYWVROTPEKRLEWVATISDDGTYTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDSVKGRFTISRDNAKNTLYLOMRSLRSEDSAMYFCT-RVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLVESGGDLVKPGGSLKLSCAASGFSFSSYGMSWVRQTPDKRLEWVATISNGGGYTYY
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                                                                                                                                                                                                                                                                                                                                                                          Sharon A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Process for Generating Specific Antibodies
72.6%;
                                                                         consensus
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Pred. No. 1.6e-41;
Score 453; DB 4;
Pred. No. 2.1e-41;
                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Length 217;
                   Length 119;
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Search completed: Decem Job time : 8.85924 secs	B &	g	Matches
)leted 8.859	61 SD 61 AD	1 EV	85;
Search completed: December 23, 2004, 19:08:01 Job time : 8.85924 secs	61 SDSVKGRFTISRDNAKWTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119 :	EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60 	85; Conservative 13; Mismatches
2004,	11170 11170 11770	SLKVSC  ::   SLRLSC	13;
19:08:01	MRSLRSEDSAMYF      :  : :   MNSLRAEDTAVYY	AASGFAFSHYAMS                AASGFTFSSYAMS	Mismatches
	CTRVKI     : CARGRY	WVRQTI	21;
	GTYYFDSWG	PAKRLEWVAY            GKGLEWVAV	21; Indels
	OGTL	TISGEC	0;
	TVSS 1	GSTYY	0; Gaps 0;
	19 19	60	0;

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Result
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-089-500-55
624
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98.4
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-10-265-713-8

US-10-166-626-8

7 US-10-06-77-37-3

US-10-06-773-4

US-10-276-939-3

US-10-281-479A-61

US-10-286-132A-61

US-10-281-479A-23
                                                                                                                                                                                               US-10-265-713-18
US-10-166-626-18
US-09-764-304-8
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Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 61, Appl
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155	144	140	125	125	137	137	118	118	118	118	118	268	268	268	262	415	268	268	268	268	262	262	262	119	119	123	123	4852	120	464	462
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US-10-077-624-7	881-823-1	US-09-286-240-4	US-09-910-358D-8	US-09-910-358D-4	US-10-337-981-76	US-09-423-800-76	-733	US-10-337-981-46	US-10-169-003-46	US-10-182-018-46	US-09-423-800-46	-328-190	•	-10-270-071-	-10-270-071-	US-10-328-190-12		-1	•	US-10-270-071-10	-10-270-071	-10-270-071-	US-10-270-071-20	US-10-270-071-6	US-10-270-071-5	US-10-632-706-58	US-09-144-886-61	US-10-412-406-33	US-10-412-406-2	US-10-275-180A-23	US-10-286-132A-23
Sequence 7, Appli	12,	Sequence 4, Appli	8	4	e 76,	76,	Sequence 46, Appl	46,	46,	•	6,	4.	Ņ	32	34		16,	14,	e 12,	e 10,	28,	24,	20	<u>ئ</u>	Sequence 5, Appli	e 58,	σ	33	ν,		Sequence 23, Appl

# ALIGNMENTS

US-09-764-304-18

Sequence 18, Application US/09764304 Patent No. US20022026036A1 GENERAL INFORMATION: APPLICANT: SHITARA, KENYA

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APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MANORU

APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILLING DATE: 2001-01-19
EARLIER FILLING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILLING DATE: 1995-03-21
EARLIER FILLING DATE: 1995-03-21
EARLIER FILLING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1991-09-18
NUMBER: OF SEQ ID NOS: 19
SOFTWARE: PATENCHIAN DATE: 1991-09-18
NUMBER: OF SEQ ID NOS: 19
SOFTWARE: ARTERITION: CDNA KM-641
US-09-764-304-18
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US-10-166-626-18
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US-10-265-713-18
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US-10-265-713-18
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PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
                                                       Sequence 18, Application US/1016626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 130
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Best Local Similarity
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Best Local
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APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HASBGAWA, MAMORU
APPLICANT: MIYAJI, HONAKA
APPLICANT: KUWANA, YOSHHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
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NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Pred. No. 2.6e-50;
Mismatches 0;
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Pred. No. 2.6e-50;
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SEQ ID NO 18
SEQ ID NO 18
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-764-304-8
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US-10-166-626-18
                                                                                                                                                                                                                                                                 FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER APPLICATION NUMBER: US 07/947,674
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR APPLICATION NUMBER: US 08/202,178
PRIOR PILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PRIOR DATE: 1992-09-17
PRIOR PRIOR PRIOR DATE: 1992-09-17
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; SEQ ID NO 8
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
                                                                                                                                                           EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.0
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                               LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FEATURE:
OTHER INFORMATION: CDNA KM-641
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Pred. No. 2.6e-50;
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US-10-265-713-8
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PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1992-09-17
                                  GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
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                                                                                                                          Sequence 8, Application US/10166626 Publication No. US20030166876A1
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Best Local Similarity
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Best Local Similarity
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APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-09
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                       EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAGISSGGSGTYY 70
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MIYAJI, HIROMASA
KUWANA, YOSHIHISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 614; DB 14; Length 130; Pred. No. 2.2e-49;
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                                                                                                                                                                                                                                                  ; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-477-377-3
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US-10-166-626-8
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR PILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR PILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR PILING DATE: 1995-03-17
PRIOR PILING DATE: 1995-09-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1991-09-18
PRIOR FILING DATE: 1991-09-18
                                                                                                                                                Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                       SOPTWARE: FastSEQ for Windows Version SEQ ID NO 3
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APPLICANT: Tornetta, Mark
APPLICANT: Tornetta, Mark
APPLICANT: Wattam, Trevor
TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
TITLE OF INVENTION: Useful in Treatment of RANK Ligand Mediated
                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: GP50050
CURRENT APPLICATION NUMBER: US/10/477,377
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US02/14246
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 60/292,031
PRIOR APPLICATION NUMBER: 60/292,031
PRIOR FILING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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Local Similarity 99.2%;
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61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
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                                                                                                                                                Similarity 79.3
96; Conservative
                                                 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                             EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
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                                                                                                                                                                       78.0%;
                                                                                                                                             Score 487; DB 17;
Pred. No. 1.4e-37;
6; Mismatches 17;
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Pred. No. 2.2e-49;
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US-10-276-939-3
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US-10-006-773-4
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Publication No. US20020132983A1
GENERAL INFORMATION:
APPLICANT: Junghans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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LENGTH: 140
Query Match
Best Local Similarity
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Best Local (
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APPLICANT: SWEET, RAYMOND W.
APPLICANT: TAYLOR, ALEXANDER H.
APPLICANT: TAYLOR, ALEXANDER H.
APPLICANT: WATTAM, TREVOR A.
TITLE OF INVENTION: Uneful in Treatment of RANK Ligand Mediated Disorders
FILE REFERENCE: GP50024
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CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/276,939
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: PCT/US01/16865
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
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PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                                                                            TYPE: PRT
ORGANISM: Murine
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ORGANISM: Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
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77.1%;
78.5%;
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Score 481; DB 14;
Pred. No. 4.7e-37;
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              APPLICANT: The UAB Research Foundation APPLICANT: Zhou, Tong
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-61
                                                                         RESULT 11
US-10-275-180A-61
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US-10-281-479A-61
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
Type. no.
Sequence 61, Application US/10275180A Publication No. US20030190687A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Buchabaum, Donald J.
APPLICANT: Buchabaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: PACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
TILLE OF INVENTION: AGENTS
TILLE OF INVENTION: AGENTS
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: FO/346,402
PRIOR APPLICATION NUMBER: POT/US01/14151
PRIOR APPLICATION NUMBER: POT/US01/14151
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
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Local Similarity 79.8%;
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Ichikawa, Kimihisa
Ichikawa, Kimihisa
Kimberly, Robert P.
Koopman, William J.
Oshumi, Jun
Oshumi, Jun
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Pred. No. 1.7e-36;
3; Mismatches 21
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Zhou, Tong Ichikawa, Kimihisa

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APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: LoBuglio, Albert S.
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U7
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 102
NUMBER OF SEQ ID NOS: 102
COCETUANDE: NEGETIAN 1 0
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
Type: """
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SEQ ID NO 61
LENGTH: 119
TYPE: PRT
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Best Local :
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Publication No. US20030198637A1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
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TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
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ORGANISM: Artificial Sequence
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                                       SDSVKGRFTISRDNAKNTLYLOMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                            EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
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PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMITTDYWGQGTTLTVSS 119
                                                                                   EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 60
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llarity 79.8%;
Conservative
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79.8%;
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Pred. No. 1.7e-36;
3; Mismatches 21;
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Pred. No. 1.7e-36;
3; Mismatches 21;
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APPLICANT: ORDING: Jun
APPLICANT: LOBUGISO, Albert S.
APPLICANT: LOBUGISO, Albert S.
APPLICANT: LOBUGISO, Albert S.
APPLICANT: LOBUGISO, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 2105.0029U6
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR APPLICATION NUMBER: 60/394,478
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-15-02
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR APPLICATION NUMBER: DCT/US01/14151
PRIOR APPLICATION NUMBER: DCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
COCUMENT OF SEQ ID NOS: 102
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US-10-281-479A-23
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US-10-281-479A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/10286132A Publication No. US20030198637A1 GENERAL INFORMATION:
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: LOBUGIIO, Albert S.
APPLICANT: LOBUGIIO, Albert S.
APPLICANT: Buchsbaum, Donald J.
APPLICANT: APPLICATION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APPLICATION NUMBER: US/10/286,132A
CURRENT APPLICATION NUMBER: US 60/346,402
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR APPLICATION NUMBER: DCT/US01/14151
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhou,
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95; Conserv
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Kimberly, Robert P.
Koopman, William J.
Oshumi, Jun
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APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberty, Robert P.
APPLICANT: Koopman, William J.
TITLE OF INVENTION: ANNIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
TITLE OF INVENTION: INDICING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U5
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
SEQ ID NO 23
LENCTH: 464
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
OTHER INFORMATION: Synthetic Construct
US-10-275-180A-23
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US-10-275-180A-23
; Sequence 23, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
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Search completed: December 23, 2004, 19:35:48 Job time: 28.0707 secs
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US-10-286-132A-23
                                                                                                                                                                                                                                                                       Query Match 76.1%; Score 475; DB 14; Length 464; Best Local Similarity 79.8%; Pred. No. 6.8e-36; Matches 95; Conservative 3; Mismatches 21; Indels
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
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Best Local Similarity 79.8%;
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    $; Score 475; DB 14; Length 462
    $; Pred. No. 6.8e-36;
    3; Mismatches 21; Indels

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Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: $5556
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin ant utations in the variable region genes.
A;Reference number: $55528; MUID:95239763; PMID:7536850
A;Accession: $55536
                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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anti-peptide Fab' B1312 heavy chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 23-Jul-1999
C;Accession: B34353
R;Stura, E.A.; Stanfield, R.L.; Fieser, T.M.; Balderas, R.S.; Smith, L.R.; Lerner, R.J.
J. Biol. Chem. 264, 15721-15725, Pieser, T.M.; Balderas, R.S.; Smith, L.R.; Lerner, R.J.
A;Title: Preliminary crystallographic data and primary sequence for anti-peptide Fab'
A;Reference number: A34353; MUID:89359424; PMID:2504725
A;Accession: B34353
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-119 <STU>
                                                             ;14-97/Domain:
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                                                          immunoglobulin homology <IMM>
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Pred. No. 1.3e-37;
8; Mismatches 18
   Score 471;
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A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin utations in the variable region genes.

A;Reference number: S55528; MUID:95Z39763; PMID:7536850

A;Accession: S55537

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X8Z590; NID:g854306; PIDN:CAA57926.1; PID:g854307
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin f;144-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

RMBO J. 5, 1577-1587, 1986

A;Title: Structural and functional implications of a restricted antibody response in A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Recession: I27887

A;Recidue type: DNA

A;Residues: 1-121 <CAT>

A;Experimental source: strain Balb/c

A;Experimental source: strain Balb/c

A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza v.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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127887

Ig heavy chain V region (H37-45) - mouse
C;Species: Mus muscullus (house mouse)
C;Acte: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change :
C;Accession: 127887
R;Caton, A.J.; Brownlee, G.G.; Standf. T. M. Gorbard "
                                                                                                                                                                                                                                                                                 Ig heavy chain V region pe21 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C;Accession: S5537
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
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76.9%;
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Score 469; DB 2;
Pred. No. 1.1e-36;
5; Mismatches 19
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the pro
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1007
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-111 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Kuywords: heterotetramer; immunoglobulin ho
C;Kcywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Reference number: A910-
A;Accession: E27888
A;Molecule type: DNA
A;Residues: 1-122 <CAT>
                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (clone 163-c1) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996 C;Accession: PH1007
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A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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E27888
Ig heavy chain V region (H35-C6) - mouse
Ig heavy chain V region (H35-C6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
C;Accession: E27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
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                        EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPAKRLEWVAYISSGGGSTYY
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Pred. No. 1.1e-36;
                                                                                                     Score 467; DB 2;
Pred. No. 1.5e-36;
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 29-Uan-1993 #sequence_revision 29-Uan-1993 #text_change 23-Jul-1999
C; Accession: S09258
R; Hamada, H; Maezawa, K; Tsuruo, T.
Nucleic Acids Res. 18, 1900, 1990
A; Title: Nucleotide sequences of the variable regions of a mouse monoclonal as A; Reference number: S09258; MUID:90245594; PMID:2110659
A; Accession: S09258
A; Molecule type: DNA
A; Residues: 1-138 <HAM>
A; Residues: 1-138 <HAM>
A; Introns: 16/1
C; Genetics:
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
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A,Residues: 1-119 <CRT>
A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Species: Mus musculus (house mouse)
pate: 29-Jan-1993 #sequence_revision 29-Jan-1993 #
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;Species: Mus musculus (house mouse)
;Date: 15-Dec-1988 #sequence_revision
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Best Local :
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PDSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYRYEAWFASWGQGTLVTVSA 138
                         SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                              EVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGGNTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY---FDSWGQGTTLTV 117
                                                                                                                     EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSYTYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCASHYYGSRTYYFDYW 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                 Conservative
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                                                                                                                                                                                  74.48;
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76.9%;
                                                                                                                                                           Score 464; DB 2; L
Pred. No. 3.7e-36;
7. Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 466.5; DB 2
Pred. No. 1.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                     Length 138;
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R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cycle A;Reference number: PH0087, MUID:91042649; PMID:2122240
A;Accession: PH0097
            Ig heavy chain V region - mouse
C;Species: Mus musculus (house
C;Date: 20-Feb-1995 #sequence_x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;15-98/Domain: F;31-35/Region: F;50-66/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X82593; NID:g854312; PIDN:CAA57929.1; PID:g854313 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin E;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining IF;50-66/Region: complementarity-determining IF;99-105/Region: compleme
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A; Residues: 1-118 <SC
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                                                                                                                                      S20641
                                                                                                                                                                      RESULT
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYIMSWVRQTPEKRLEWVATISSGGRYTYY
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Pred. No. 4.3
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Pred. No. 3.9e-36;
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20-Feb-1995 #text_change 23-Jul-1999
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C;Accession: $20641
R;Iosman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune
A;Reference number: $20639
A;Accession: $20641
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <LOS>
A;Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: immunoglobulin homology <IMM>
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F;50-66/Region:
F;67-98/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)

(;Species: Mus musculus (house mouse)

C;Date: 16-Sep-192 #sequence_revision 16-Sep-192 #text_change 16-Aug-1996

C;Accession: PL0249

C;Accession: PL0249

A;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Recession: PL0249

A;Molecula type: mRNA
A;Residues: 1-11 <SHL-
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1
Ig heavy chain V region pe22 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55538
C;Accession: S55538
C;Accession: S55538
B;Boettger, V: Boettger, A.; Lane, B.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
J. Mol. Biol. 247, 932-946, 1995
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Matches 88
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||||||||||||:|||
PDSVKGRFTISRDNVMNILYLQMSSLRSEDTAMYYCARRAYSNYALDFWGQGTSVTVS 118
                                                                                                                                                                                                                                                                  PDSVKGRFTISRDNARNTLYLQMSSLRSEDTAVYYCARRDYSHWFFDVWGAGTTVTV 117
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llarity 75.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 461; DB 2; 1
Pred. No. 5.9e-36;
8; Mismatches 21;
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Pred. No. 4.8e-36;
monoclonal anti-proenkephalin antibodies
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C;Accession: PH0096

R;Schmitter, D.; Pooch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesnia Mol. Immunol. 27, 1029-1038, 1990

A;Title: Analysis of the structural diversity of monoclonal antibodies to c A;Reference number: PH0087; MUID:91042649; PMID:2122240

A;Accession: PH0096

A;Molecule type: mRNA

A;Residues: 1-118 <SCH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Muyords: heterotetramer; immunoglobulin C;Feywords: heterotetramer; immunoglobulin P;15-99/Domain: immunoglobulin homology <IMM>
F;15-99/Domain: immunoglobulin homology <IMM>
F;11-35/Region: complementarity-determining 1
F;90-66/Region: complementarity-determining 3
F;99-105/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 2
C;Accession: B31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, B.A.; Kente
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and
A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: B31790
A;Molecule type: mRNA
A;Residues: 1-254 <SCH>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55538
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82591; NID:g854308; PIDN:CAA57927.1; PID:g854309
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (anti-cyclosporin A) - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #t
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Similarity 75.8%;
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Pred. No. 2.8
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Pred. No. 7.5e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8e-35
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Result
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: uniprot_trembl:*
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<pre>F; 255 AA. eed) sequence update) annotation update)</pre>	tches 17; FSHYAMSWVRQTP                       FSSYGMSWVRQTP SSYGMSWVRQTP EDSAMYFCTRVKL                     EDTAMYYCAR-HI	nk/DDBJ da	55 AA. nce update) ation update) ; Vertebrata; athi; Muridae;	STIN.
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RA Strausberg R.I., Feingold E.A., Grouse L.H., Derge J.G.,

K.Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

K.Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

K.A. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

K.A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

K.A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

K.A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

K.A. Landers M.J., Bendlow M.F., Rubin G.M., Hong L.,

K. Carantoni P., Prange C.,

K. Stapleton M., Ugdin T.B., Donaldo M.F., Carannori P., Prange C.,

K. Stapleton M., Ugdin T.B., Donaldo M.F., Carannori P., Prange C.,

K. Brownstein M.J., Ugdin T.B., Donaldo M.F., Abramson R.D., Mullahy S.J.,

K. Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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K. Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

K. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

K. Willing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

K. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

K. K. Shein J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

K. A. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

K. Jones S. J., Marra M.A.,
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
"Generation and initial analysis of more than 15,000 and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary tumor metastatized to lung. Tumor arose MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-M2 receptor antibody fragments.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AJ746180; CAG34081.1; -.
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Briand J.P., Hoebeke J.;
"Modulation of the M2 muscarinic receptor
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl.set; 2.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IG HC; UNKNOWN 2
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Q920E7;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 1.

NON TER 1 1 19

NON TER 119 119

SEQUENCE 119 AA; 13025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF307937; AAL09421.1; PIR; C25913; C25913. HSSP; P01783; 1IGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atkin J.D., Iape A., Submitted (SEP-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC004786; AAH04786.1; -
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Mammary tumor metastatized Strausberg R.;
                                                                                                                                                                                                                                                                                                                Pfam; PF00047; : SMART; SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pterin-mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; InterPro; IPR003596;
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                                                                                                                                                                                                                                                                                                                                     PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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                                                                                                                                                          Similarity
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SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS
                                                                       EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDNVKGRFTISRDNAKNNLYLQMSHLKSEDTAMYYCARDMGGSPYGGYSRFDYWGQGTTI
                                           EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSVTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISDGGSYTYY
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TIRMBLrel. 19, Created)
(TIRMBLrel. 19, Last sequence update)
(TIRMBLEL. 25, Last annotation updat)
Cking anti-idiotope heavy chain variab
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                                                                                                                                                                                                                                                                                                                   IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                           13025 MW;
                                                                                                                                                                                                                                                                                                                                                     Ig-like.
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75.0%;
                                                                                                                                                      74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jennings I.G., Horaitis (
to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                   6;
                                                                                                                                   Score 463; DB 2;
Pred. No. 7.8e-41;
6; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 468.5;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                           F6E904044381CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WN 2.
7DC8E96DB333077B CRC64;
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n variable
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J databases.
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                                                                                                                                                                             Length 119;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
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RESULT
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RC Expression driven by an MMTV-LTR enhancer;

RX MEDLINE-22388257; PubMed=12477932;

RX MEDLINE-22388257; PubMed=12477932;

RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Peingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Uddin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McCEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,

RA Hhitring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J. - Marra M.A.,
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                                                                                                                        Query Match
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF07654; Cl-set; 2.
Pfam; PF07654; Ig; 1.
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TISSUE-Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
Expression driven by an MMTV-LTR enhancer.;
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LOC38091 protes.

Mus musculus (Mouse).

Metazoa; Chordata;

Metazia; Rodentia;
                                                                                                                                                                                                                                       SMART; SMO0406; IGV; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG_MHC; UNKN
SEQUENCE 486 AA; 52681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC010324; AAH
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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20
                                                                                                                                                     Similarity
                             EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S 119
EVHLVESGGGLVKPGGSLKLSCVVSGFSFTSYDMSWVRQTPERRLEWVAAITSGGN-TYY
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                                                                                                                                                     72.9%;
                                                                                                                                                                                                                                       UNKNOWN 2.
MW; 4FEF835125DA870B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
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                                                                                                                 Score 455; DB 2;
Pred. No. 2.7e-39;
4; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                   Query Match
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Matches 88
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XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Holder M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Kones S. T. Mayers M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Kones S. T. Mayers M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                          Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC013656; AAH13656.1; -.

HSSP; P01789; IMCP.
InterPro; IPR0077110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; Cl-set; 2.

Pfam; PF07654; Cl-set; 2.

Pfam; PF00047; Ig; 1.
SMART; SM00406; IGy; 1.
SMART; SM00406; IGy; 1.
SMART; SM00406; IG_HC; UNKNOWN 2.
SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91WP5; PRELIMINARY;
Q91WP5; PTEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ن
19
    13
                                       20
                                                                                                                                        Similarity
SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTFAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY-----YFDSWGQGTTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDNVKGRFTVSRDNAKYTLYLOMSSLKSEDTAMYYCVRPEIPIYYYSGSYFDSWGQGTTI 138
                                       EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prote
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                      72.1%;
                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                   Score 450; DB 2;
Pred. No. 8.9e-39;
9; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                     18;
                                                                                                                                                        Length
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length humar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae; Mus.
                                                                                                                                                             479
                                                                                                                   4
                                                                                                                   Gaps
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SDIMKGRPTISRDNAKSTLYLQMSSLRSEDTAFYYCVR----GGYPDVWGAGTAVTVSS

134

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                                                                         Query Match
Best Local S
Matches 86
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Kasavant T.L., Scheetz T.E.,

Bistelenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bisteley S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Halkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S. T. Mayra M.A., A Jones S. J. Ma
                                                                                                                                                                                                                                                                                                   MGD; MGI:2144967, AU044919,
InterPro; IPR000345; CyrC heme_BS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007597; Ig-c1.
InterPro; IPR003597; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
IfterPro; IPR003596; Ig-MHC.
IfterPro; IPR003596; Ig-MHC.
IfterPro; IPR003596; Ig-MHC.
IfterPro; IPR003596; Ig-MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;

"Generation and initial analysis
and mouse cDNA sequences.";

"""" Acad. Sci. U.S.A. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "ISSUE=Mammary tumor metastatized to Expression driven by an MMTV-LTR enha MEDLINE=22388257; PubMed=12477932; Stransherr B T. Friends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC010327; AAH10327.1;
PIR; S68213; S68213.
HSSP; P01783; 1IGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001
01-MAR-2004
                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Mammary tumor 
Expression driven by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CZECH II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CZECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=AU044919;
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L-DEC-2001 (TrEMBLrel. 19, Last sequence update)
L-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                         96;
                                                                                               Similarity
                                                                                                                                                               PS00190; CYTOCHROME_C; UNKNOWN_1.
PS50835; IG_LIKE; 4.
PS00290; IG_MC; UNKNOWN 1.
473 AA; 51946 MW; CF625F008932AF12 CRC64;
EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence AU044919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JUL-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                               70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastatized to lung. MMTV-LTR/Wnt1
an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases.
                                                                     Score 439.5; DB 2
Pred. No. 1.1e-37;
0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d to lung.
enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              more than 15,000 full-length human
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                                                                                                                    DB 2;
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                                                                         22;
                                                                         Indels
                                                                                                                  Length
                                                                                                                    473;
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Best Local S
Matches 82
                      NON_TER
                                                                                                                                                                                                                                                                                                                                         BAD00534;
02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
10-MAR-2004 (TrEMBLrel. 27,
                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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02-MAR-2004
                                                                                    gamma3 in vivo repertoires."
Submitted (SEP-2002) to the I
                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                            IGVH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAD00534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma3 in vivo repertoires."
Submitted (SEP-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Honda T., Akahori Y., Kurosawa Y.; "Libraries of heavy-chain antibodies reflecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGVH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2004
02-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAD00406
  SEQUENCE
                                                                                                                              Honda T., Akahori Y., Kurosawa Y.;
"Libraries of heavy-chain antibodies
                                                                                                                                                                      TISSUE=Spleen;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                    Camelus dromedarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Camelus dromedarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin
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                                                                  AB092172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB092044; BAD00406.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNAKNTLYLQLNSLKTEDTAMYYCAKDRYGGRWLSGDYSMDYWGKGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLVESGGGLVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSTTIYY
124
124
                                                                                                                                                                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
128 /
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  A,
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                                                                  BAD00534.1;
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13856 MW;
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Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                                                                                                                                                                                                                                          (Dromedary) (Arabian camel).
Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Tylopoda; Camelidae; Camelus
    13421
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    Æ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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, Last annotation update)
VHDJ region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHDJ region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 438; DB
Pred. No. 3.6e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
    B31996777375A27E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7C23CF09C28B8B9A CRC64;
                                                                                                                              reflecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
.6e-38;
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RESULT 11
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ID AAL35
AC AAL35
DT 02-M2
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DT 102-M3
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Best Local &
Matches 81
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Best Local :
AALJ5877 PRELIMINARY; PRT; 117 AA.
AALJ5877;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Immunoglobulin heavy chain variable domain (Fragment).
Lama glama (Llama).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
NCBI TaxID=9844;
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NON_TER
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SEQUENCE
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"Libraries of heavy-chain antibodies reflecting camel gamma2 and gamma3 in vivo repertoires.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB092129; BAD00491.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
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ilarity 67.2%;
Conservative 1
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llarity 66.9%;
Conservative 1
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Pred. No. 1.1e-37
(8; Mismatches 1)
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.anha J., Dubuc G., Hirama T., Narang S.A., MacKenzie C.R.;
RT "Selection by phage display of llama conventional V(H) fragment:
RT heavy chain antibody V(H)H properties.";
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AP442946; AAL35877.1; --
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NON TER 117 117
SEQUENCE 117 --
RESULT PACKET AND RESULT ROCKET PACKET PACKE
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WEDLINE-22386357; PubMed=12477932;

Richausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Richausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Richausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Richaushi S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Richaushi S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Richaushi S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Richaushi S., Royale R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Richaushi M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richaushe S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Raha S.S., Loquellano B., Ketteman M., Wadan A., Gay L.J., Sanchez A.,

Raha S.S., Loquellano B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Raha S.S., Loquellano B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Raha S.S., Loquellano B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Raha S.S., Loquellano B., Ketteman M., Madan A., Gay L.,

Raha S.S., Loquellano B., Ketteman M., Madan A., Gay L.,

Raha S.S., L
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                          SEQUENCE FROM N.A.

TISSUE=Primary B-Cells;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EME
Submitted (JUN-2004) to the EME
EMBL; BC073758; AAH73758.1; -.
InterPro; IPR003599; Ig.-like.
InterPro; IPR003597; Ig.-cl.
InterPro; IPR003596; Ig.-MCC.
InterPro; IPR003596; Ig.-WC.
InterPro; IPR003596; Ig.-WC.
InterPro; IPR003596; Ig.-WC.
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Q6GMY2;
Q5GMY2;
05-JUL-2004 (TrEMBLrel
05-JUL-2004 (TrEMBLrel
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Ch.
Mammalla; Eutheria; Pr.
   Pfam;
Pfam;
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c. Natl. Acad. Sci. U.S.
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4 (TrEMBLrel. 27,
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Primates;
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Pred. No. 1.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                       99:16899-16903 (2002)
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Best Local S
Matches 82
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Best Local Similarity 64.2
Matches 86; Conservative
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01-NOV-1990
15-JUL-1999
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NON TER
SEQUENCE
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DOMAIN
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SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG LIKE; 1.
PROSITE; PS50815; IG LIKE; 1.
                                                                                                                                                                                                              PIR, JT0502; HVMS34.
HSSP; P01783; 1IGC.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 4.
SMART; SM00400; IGC; 1.
SMART; SM004006; IGC; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS508290; IG_MHC; UNKNOWN_3.
                                                                                                                                                          SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                       STRAIN=BALB/CJ;
MEDLINE=89279149; PubMed=2499654;
Levy N.S., Maliplero U.V., Lebecque
Levy N.S., Maliplero mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                          "Early onset of somatic mutation primary immune response.";
J. EXP. Med. 169:2007-2019(1989).
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mus musculus (Mouse)
                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                Similarity
          EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
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EVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTPEKRLEWVAYISSGGGSTYY
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(Rel. 16, Last sequence update)
(Rel. 38, Last annotation update)
ain V region 345 precursor.
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49
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Rodentia;
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                                             69.1%;
83.7%;
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                                                                                                                                                                            Signal.
                                                                             WW;
                                    Score 431; DB; Pred. No. 1.8e
5; Mismatches
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Pred. No. 1e-3
L3; Mismatches
                                                                                             Pramework-2.
Complementarity-determining-2.
Framework-3.
By similarity.
                                                                                                                                    Ig heavy chain V region 345. Framework-1. Complementarity-determining-1.
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Sciurognathi; Muridae;
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                                                                            49380E4627ACA99A CRC64;
                                                                                                                                                                                                                                                           belongs
                                                                                                                                                                                                                                                                                      S.G., Gearhart
immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                          117
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                                    DB 1; I
l.8e-37;
les 11;
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VH genes
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; Murinae; Mus
                                                         117;
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                                     Gaps
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RESULT 15
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AC Q91XE
AC Q91XE
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-MA
DB 1gh-V
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OC Mamma
OC Mamma
OC Mamma
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RP SEQUE
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Best Local S
Matches 82
                                                                                                                                      Q91XE1;
Q91XE1;
01-DEC-2001
01-DEC-2001
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Q9UL71;
01-MAY-2000
01-MAY-2000
01-OCT-2003
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NON TER
SEQUENCE
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Gr
Klausner R.D., Collins F.S., Wagne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
                                                                                                      ign-vJ558 protein
Name=Igh-vJ558;
                                                                                                                           01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; : SMART; SM00406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                              NCBI_TaxID=10090;
                                                                                             Mus musculus (Mouse)
                                                                                                                  Igh-VJ558
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; SM00406; IGV; 1.
TE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                             S 119
                                                                                                                                                                                                                                                                            SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY--FDSWGQGTTLTVS
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IPR003596; Ig_v.
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121 AA;
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                                                                                                                 (Fragment).
                                                                         Chordata;
Rodentia;
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25,
 B.A., Grouse L.H., Derge J.C
S., Wagner L., Shenmen C.M.,
                                                                                                                                                                                                                                                                                                                                                    14;
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Pred. No. 2.4e
14; Mismatches
                                                                                                                            Last sequence update)
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Catarrhini; Hominidae;
                                                                         Craniata; Vertebrata; | Sciurognathi; Muridae;
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             J.G.,
                                                                                     Euteleostom1;
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   Schuler
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Search completed: December 23, 2004, 19:04:39 Job time: 34.1041 secs
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Alpokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Alpokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Alpokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Alpokins R.F., Jordan H., Moore T., Max R.A., Rubin G.M., Hong L.,
Alpokins R.F., Loquellan B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Alpokins R.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Alpokak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Alpokins R.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
Alpokins R.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hillyk S.W.,
Alpokins R., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Alpokins R.S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Alpokins R. W., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Alpokins R. W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Alpoke S. J. Marra M.A., Alpoka U., Smailus D.E., Schnerch A., Schein J.E.,
Alpoke S. J. Marra M.A., Alpoke S
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Best Local S
Matches 85
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; 2.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; PS00290; IG_MHC; UNKNOWN_2.
NON TER
SEQUENCE 480 AA; 51936 MW; 20B92341
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STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
HSSP; P01789; IMCP.
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                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                 61 SDSVKGRFTISRDNAKNTLYLOMRSLRSEDSAMYFCTRVKLGTY-YFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                         19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.8%; Score 429; DB 2; Length 480; 70.8%; Pred. No. 1.5e-36; Live 13; Mismatches 18; Indels
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GenCore version (c) 1993 - 2004

5.1.6 Compugen Ltd

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Minimum
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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572
1 DIQMTQTASSLPAS
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1340.986 Million cell updates/
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ABU11013
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Aaw16620
Aaw16620
Aab81998
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Adn41870
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Gangliosi

Anti-CD7

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45	44	43	42	41	40	39	38	37	36	35	ω 4	ω ω	32	31	30	29	28	27	26
488	488	488	490	490	490	490	490	491	491	494	495	497	497	497	498	499	500	501	502
85.3	85.3	85.3	85.7	85.7	85.7	85.7	85.7	85.8	85.8	86.4	86.5	86.9	86.9	86.9	87.1			87.6	
107	107	107	109	107	107	107	107	107	107	108	119	128	109	109	112	128	131	128	131
æ	9	N	æ	8	7	σ	N	9	σ	4	œ	4.	6	4	4	4	ထ	4	N
ADN49724	ABR55867	AAW49812	ADG25821	ADH50840	ADC84579	AA027199	AAW66098	ABJ18574	ABJ18571	AAB81986	ADM78045	AAB81993	ABP72768	AAB62050	AAE00697	AAB81996	ADI26634	AAB81997	AAR84553
Adn49724 Variable	Abr55867 Anti-glyc	Aaw49812 Amino aci	Adg25821 Anti-CD30	Adh50840 Mouse ant	Adc84579 CDR3 heav	Aao27199 Murine an	Aaw66098 anti-CD22	Abj18574 Gangliosi	Abj18571 Gangliosi	Aab81986 Gangliosi	Adm78045 Human SKB	Aab81993 Gangliosi	Abp72768 Anti-full	Aab62050 Mouse mor	Aae00697 Human imm	Aab81996 Gangliosi	Adi26634 Human ant	Aab81997 Gangliosi	Aar84553 MAb SCH94

ALIGNMENTS

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CC Gequ 30-SEP-1999; 99JP-00278291. 06-APR-2000; 2000JP-00105088. 29-SEP-2000; 2000WO-JP006774 05-APR-2001. WO200123432-A1 Mus musculus. cancer. Ganglioside; GD3; complementarity determining region; CDR; antibody; Ganglioside 03-JUL-2001 AAB81990; AAB81990 standard; GD3 (first entry) specific protein; antibody related 108 ጅ protein SEQ ij NO: 56

(KYOW ) KYOWA HAKKO KOGYO KK

Hanai N, Shitara K, Nakamura ζ, Niwa

WPI; 2001-266143/27.

New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent

in cancer.

The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention Claim 11; Page 174-175; 183pp; Japanese.

Sequence 108 Å,

Query Match Best Local Similarity Matches 108; Conservative 100.0%; bu 100.0%; Pr Score 572; DB 4; Pred. No. 3.3e-39; ; Mismatches 0; Length 108; Indels 0 Gaps 0

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RESULT 2
ABUII 13
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reaction, particularly to relieve problems of side-effects during the conventional single administration. This sequence represents a protein associated with the anti- ganglioside GD3 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drugs containing genetically-modified antibody against ganglioside GD3, its fragment, immunocompetent cell activators or/and antitumor agents i combination, applicable in treating malignant tumor like melanoma.
                                                             AAB01628 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified ganglioside GD3 antibody associated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
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                                                             protein; 128
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Pred. No. 3.3e-39;
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                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                The present sequence is a murine immunoglobulin light chain variable region from plasmid KM-641. The coding sequence was used in the creation of an expression vector, along with the sequence for a human antibody, to produce humanised chimaeric antibodies, which can be used to treat cancer. Humanised chimaeric antibodies are more effective than mouse antibodies as they do not provoke a reaction in the human and side effects, such as the formation of anti-mouse immunoglobulin antibody and the rapid half-life of the immunoglobulins, do not occur
                                                                                                                                                                                                                                                                                                            Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized chimera antibody KM-871 useful for treating cancer, comprises variable region of mouse monoclonal antibody, reactive with
                                                                                                 AAB81978 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 28-29; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ganglioside and human antibody constant
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18-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-1992;
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                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                    RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
                                                                                                                                                                                                             DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                                                                                               RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
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                                                                                                                                                                                                                                                              Conservative
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92EP-00116026.
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/label=_signal_peptide
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                                                                                                protein;
                                                                                                                                                                                                                                                                        100.0%;
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Ganglioside; GD3; complementarity determining region; CDR; antibody;

specific antibody related protein SEQ ID NO:

Ganglioside GD3 03-JUL-2001

(first entry)

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therap of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                 Ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                  Modified
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06-APR-2000;
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                        Niwa
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Pred. No. 3.9e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour like melanoma and can provide a treatment with enhanced therapeutic effect and little side-reactions, particularly to relieve problems of side-effects during the conventional single administration. This sequence represents a protein associated with the anti- ganglioside GD3 antibody
                     This immunoglobulin region was isolated from pKM641LA2. A methionine codon, presumably the initiation codon ATG, was found in the vicinity the 5' terminus and the sequence has a full length leader sequence. The chimeric human antibodies are useful in the treatment of cancer, especially that which is of neural ectodermal origin. In contrast to
                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drugs containing genetically-modified antibody against ganglioside GD3 its fragment, immunocompetent cell activators or/and antitumor agents combination, applicable in treating malignant tumor like melanoma.
                                                                                                                          Chimeric human
                                                                                                                                                                                       Nakamura K,
                                                                                                                                                                                                                                          07-SEP-1993;
                                                                                                                                                                                                                                                                                            17-AUG-1999.
                                                                                                                                                                                                                                                                                                                                              Mus
                                                                                                                                                                                                                                                                                                                                                                      antibody; nucleotide; genomic;
light chain; amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                            PKM641 LA2
                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY28368 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 98; 121pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-067410/06
                                                                                                  Example
                                                                                                                                                                                                                  (KYOW)
                                                                                                                                                                                                                                                                                                                    US5939532-A.
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                                                                                                                                                               1999-468416/39
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                                                                                                 1; Col 99; 188pp;
                                                                                                                                                                                                                  KYOWA
                                                                                                                                                     AAX99481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQTASSLFASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                       Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                  HAKKO
                                                                                                                          antibody expression
                                                                                                                                                                                                                                          93US-00116778
                                                                                                                                                                                                                                                                   95US-00483528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                  KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                         Kuwana
                                                                                                  English.
                                                                                                                                                                                                                  Ķ
                                                                                                                                                                                                                                                                                                                                                                                                           light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
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Pred.
                                                                                                                                                                                         ĸ
                                                                                                                                                                                                                                                                                                                                                                                   hypervariable region; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                              chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                         Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e 572; DB 6;
. No. 3.9e-39;
smatches 0;
                                                                                                                           vectors
                                                                                                                                                                                         Σ,
                                                                                                                                                                                         Koike
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prior art human anti

art constructs based on mouse monoclonal antibodies, antibodies do not cause anti-mouse immunoglobulin pr

chimeric tion. The

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RESULT 7
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  Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
           Query Match
Best Local Similarity
                                                             variable regions respectively. The DNA sequences encoding these proteins were used in the construction of humanised chimeric antibody expression vectors. In these humanised antibodies none of the amino acids of the nor human animal Ab variable region have been changed. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimeric human antibodies have a prolonged half-life and a reduced frequency of adverse effects when compared to mouse monoclonal antibodies
                                                                                                                                                            Humanised chimeric antibody prodn. against ganglioside {\tt GD3} -cancers, such as melanoma, neuroblastoma, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
12-JUL-1993
                                            Sequence
                                                                                                                    The sequences given in AAR33256-57 represent rat heavy and light chain
                                                                                                                                          Claim 6;
                                                                                                                                                                                                                             Shitara K,
                                                                                                                                                                                                                                                                       18-SEP-1991;
                                                                                                                                                                                                                                                                                             18-SEP-1992;
                                                                                                                                                                                                                                                                                                                  24-MAR-1993
                                                                                                                                                                                                                                                                                                                                      EP533199-A2
                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoter; variable; region; rat; immunoglobulin; heavy; H; chain; humanised; chimeric; antibody; expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat immunoglobulin L chain varible region of pKM641LA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR33257
                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO CO LTD
   107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
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                                            128
                                                                                                                                       Page 30-31; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTSGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AA;
                                                                                                                                                                                                                             Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
  Conservative
                                           A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                       91JP-00238375
                                                                                                                                                                                                                                                                                             92EP-00116026
                                                                                                                                                                                                                                                                                                                                                                     /note= "Signal peptide" 21. .128
                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.6%;
          98.3%;
99.1%;
                                                                                                                                                                                                                             Hasegawa
                                                                                                                                                                                                                                                                                                                                                         "Mature protein"
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Score 562; DB Pred. No. 2.5e 0; Mismatches
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Pred. No. 1.7e-38;
0; Mismatches 1
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           DB 2;
.5e-38;
                                                                                                                                                                                                                              Kuwana
                    Length 128;
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 Indels
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 Gaps
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RESULT 8
AAS53340
ID AAR5
XX AAR5
XX AAR5
XX AAR5
XX MONO
XX MONO
XX MONO
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                                                                                                                                                                                                       Query Match
Best Local Sim.
Matches 106;
                                                                                                                                                                                                                                                                                                                                                          Example 2 describes the construction of the vector pChi641HAl for chimeric human antibody H chain expression. mRNA from mouse anti-CD3 monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain cDNA plated. The base sequences of the Ig variable regions in KM641 H chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in AAQ45418-39. A KM641-derived chimeric human Ab H chain expression vector was constructed by joining the H chain variable region gene from pKM641HA3 to a vector for chimeric human Ab H chain expression using the synthetic DNAs given in AAQ63439 and AAQ63440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised antibody specific for ganglioside GM2 - used for producing a cytocidal effect on cancers such as melanoma, neuroblastoma and glioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                               Sequence 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 115-116; 191pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1993;
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DB; AAQ45438.
81
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                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain variable region.
                                                                                                     RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
  RFSGGGSGTDYSLTISNLEPGDIATYFCHQYSKLPWTSGGGTKLEIKR
                                                 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                               ă,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koike M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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/label= sig_peptide
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                                                                                                                                                                                                                                  97.4%;
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                                                                                                                                                                                                          <u>,</u>
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                                                                                                                                                                                                          Score 557; DB 2;
Pred. No. 6.5e-38;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>≍
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                                                                                                                                                                                                                                                           Length 128;
                                                                                                                                                                                                            Indels
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RESULT 10
AAR12359
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AC AAR12
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DT 25-MA
DT 15-AU
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Best Local (
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                       The present sequence is the light chain variable region of the anti-human Fas ligand monoclonal antibody (MAb) NOK-1 is produced by the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma 23x63Ag8.653 (ATCC CRL-1580) cells. The MAb recognises the human Fas ligand on the cell surface or in solution, and can be used to inhibit the application inducing cell surface Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay in biological samples (e.g. human blood), especially for disease
                                                                                                                                                                                                                                                                                     Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody specifically recognising the Fas ligand -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-1995;
27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variable region; light chain; human; Fas ligand; monoclonal; antibody; NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease; hepatitis; infectious mononucleosis; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kayagaki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable light chain of anti-human Fas ligand antibody NOK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW00834 standard; protein;
25-MAR-2003
15-AUG-1991
                                       AAR12359;
                                                               AAR12359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 41; Page 93-94; 133pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9629350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1996-443140/44.
                                                                                                                               61
                                                                                                                                                       5
                                                                                                                                                                                                         -
                                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMITOMO ELECTRIC IND
                                                                                                                                                                                                DIQMIQTASSLPASIGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                                                                            RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
                                                               standard;
                                                                                                                               RESGSGSGTD
                                                                                                                                                                                DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yagita H,
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95JP-00087420.
95JP-00303492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-JP000734.
                                                               protein;
                                                                                                                         /SLTISNLEPEDIATYFCQQYSEFPWTFGGGTKLEIKR
                                                                                                                                                                                                                                             91.1%;
90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okumura K,
                                                               127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                                                               Score 521; DB 2;
Pred. No. 4.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                               ₹
                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakata
                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                          Length 108
                                                                                                                                                                                                                                   Indels
                                                                                                                               108
                                                                                                                                                       108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 solution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                  60
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밁 Ś 망 S

Mus musculus

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RESULT 11
AAW04177
ID AAW04
XX AAW04
XX 19-MA
XX Uaria
XX Varia
XX Varia
XX Varia
XX Varia
XX NOK-11
KW NOK-11
KW Varia
XX Varia
XX MAB MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the light (kappa) - chain variable (V) region of a mouse monoclonal antibody (MAD), 1C11, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAD comprising heavy and light chains having murine V regions and human C regions. The chimeric MADs are more effective than murine MAD 1C11 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MADs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. See also AAQ12056-60 and AAQ12056-63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct DR field.)
                                                    Variable region; light chain; human; Fas ligand; monoclonal; NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; dihepatitis; infectious mononucleosis; systemic lupus erythemat
                                                                                                                                 Variant variable light chain
                                                                                                                                                                         19-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric mouse-human antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-178105/24.
N-PSDB; AAQ12061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XOMA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light (kappa) chain
                                                                                                                                                                                                             AAW04177;
                                                                                                                                                                                                                                                   AAW04177 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9107493-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen from sample.
                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
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GREEN CROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIQMTQTASSLFASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                    RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                             DIQMIQTISSISASIGDRVIISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS
                                                                                                                                                                                                                                                                                                                                                  RESGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPWTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Horwitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 13; 107pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00433730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00433730
                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variable region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoconjugates; HIV; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ghoshdasti P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                   108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 520; DB 2;
Pred. No. 6.6e-35;
4; Mismatches 5
                                                                                                                                   of Fas
                                                                                                                                 ligand antibody NOK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine 1C11 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detect,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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RESULT 12
AAW16620
ID AAW16
XX AAW16
XX AAW16
XX I14-JA
XX Light
KW Hepatt
K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a variant light chain variable region of the anti-
human Fas ligand monoclonal antibody (MAb) NOK-1. NOK-1 is produced by
the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
with transformed human Fas ligand expressing COS cells, and fusing spleen
cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
cells. The MAb recognises the human Fas ligand on the cell surface or in
solution, and can be used to inhibit the apoptosis inducing cell surface
Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay
in biological samples (e.g. human blood), especially for disease
diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1995;
27-OCT-1995;
     27-OCT-1995;
                                                         24-OCT-1996;
                                                                                                                01-MAY-1997.
                                                                                                                                                                       WO9715326-A1
                                                                                                                                                                                                                                                                                                       monoclonal antibody; MAD; hybridoma; treatment; hepatitis; hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell;
                                                                                                                                                                                                                                                                                                                                                                 Light chain; variable region; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human FasL antibody (NOK1) light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW16620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody specifically recognising the Fas ligand - useful the detection of Fas ligands either on cell surface or in solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kayagaki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1996-443140/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMITOMO ELECTRIC IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPSSLSASLGDRYTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESGSGSGTDYSLTISNLEPEDIATYECQQYSEFPWTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 80-81; 133pp; Japanese
                                                                                                                                                                                                                                                                                oxaloacetate; pyruvate transaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95JP-00087420.
95JP-00303492.
     95JP-00303491
                                                         96WO-JP003089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-JP000734.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                              murine; human; Fas ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                 FasL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-human Fas ligand (Fasi) monocional antibody (MAD) NOK1, which is expressed by the hybridoma NOK1 (FERM BP-5044). The MAD can be used in the preparation of a composition for the effective oral or parenteral virus. The composition controls apoptosis in liver cells caused by the binding of Fasi to Fas expressing liver cells, and improves liver function by improving blood glutamate oxaloacetate and pyruvate transaminase levels. The composition is given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day. Spleen cells from mice immunised with Fasi expressing COS cells were fused with mouse myeloma cells to produce hybridomas. The hybridomas were screened for anti-Fasi activity, and the
           WPI; 2001-266143/27.
N-PSDB; AAF86912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the light chain variable region of the anti-human Fas ligand (FasL) monoclonal antibody (MAD) NOK1, wh
                                                                                                30-SEP-1999;
06-APR-2000;
                                                                                                                                                                                                                                      cancer.
                                                                                                                                                                                                                                                   Ganglioside;
                                                                                                                                                                                                                                                                        Ganglioside GD3 specific antibody related protein #7.
                                                                                                                                                                                                                                                                                                                           AAB81998;
                                                                                                                                                                                                                                                                                                                                                  AAB81998 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 30-31; Slpp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-human Fas Ligand antibody liver cells and improves liver
                                                Hanai N,
                                                                                                                                    29-SEP-2000; 2000WO-JP006774
                                                                                                                                                               05-APR-2001.
                                                                                                                                                                                      WO200123432-A1
                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       active clones NOK1-5 isolated
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                                                                         (KYOW)
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                                                                        куома накко
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                               Shitara K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                2000JP-00105088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                GD3; complementarity
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                             99JP-00278291
                                                                          KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.2%;
                                                  Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 516; DB 2;
Pred. No. 1.2e-34;
4; Mismatches 7
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Claim

9; Page 8; 55pp; English.

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RESULT 14
ABR62591
ID ABR62
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Best Local
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positive disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                   Key
Region
        New fusion protein comprising functionally linked components of an au CD7 antibody or its fragment and an immunotoxin, useful for treating positive acute T-cell and/or myeloid leukemias, or Graft-versus-host
                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                                  11-DEC-2002; 2002WU-EP014064
                                                                                                                                                                                                                   WO2003051926-A2.
                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR62591 standard; protein; 650
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                                                                                                                   (UYER-) UNIV ERLANGEN-NUERNBERG
                                                                     2003-523519/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in cancer.
                                                                                             Gramatzki
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                                                                                                                                                                                                                                                                                                                                                                                                          TH-69; scFv; exotoxin A; immunotoxin; cytostatic,
                                                                                                                                                                                                                                        /label= ETA
                                                                                                                                                                                                                                                     /label= Linker
286. .646
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Pred. No. 1.4e-34;
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The present sequence is that of a novel fusion protein comprising an scfv CC fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of CB Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including CC an N-terminal 6xHis tag and C-terminal KDEL sequence. This novel fusion protein binds to CD7-positive T-lymphoid cells and kills them by the CC induction of apoptosis. It is an example of anti-CD7 scfv immunotoxin CC fusion proteins of the invention. An expression vector, host cells, a CC method for producing the fusion protein, and a vaccine comprising the CC fusion protein are claimed. The fusion protein is used in the treatment CC of disorders involved a hyperproliferation of CD7-positive cells, cC especially acute T-cell and/or myeloid leukaemia, and also in the CC treatment or prophylaxis of Graft-versus-host disease. A claimed method CC conditioning an animal (e.g. a human) be transplanted with donor CC cells, tissue or organ comprises: (a) depleting the CD7-bearing cell population in (a) and/or the transplant CC donor, where the CD7-bearing cell population in (a) and/or the transplant CC protein or therapeutic composition comprising the fusion protein; and (c) introducing the transplant of the fusion or therapeutic composition comprising the fusion protein; and (c)
Sequence 650
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          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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                                                         1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                             DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS
                                                                                            Mismatches
                                                                                            Indels
                                                                                            0;
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Matches Query Match

Local

Similarity

90.2%;

Score 516; DB 6; Pred. No. 7.1e-34;

Length 650;

Conservative

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ABR62590
ID ABR6
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XX ADT 06-N
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Region
                                                                                                                       11-DEC-2002; 2002WO-EP014064
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Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein.
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286. .646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= scFv
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14-DEC-2001; 2001US-0339422P

(UYER-) UNIV ERLANGEN-NUERNBERG

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The present sequence is that of a novel fusion protein comprising an scFv CC fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of CP seudomonas exotoxin A (ETM), joined via a peptide linker, and including CC an N-terminal 6xHis tag and C-terminal REDLK sequence. This movel fusion CC protein binds to CD7-positive T-lymphoid cells and kills them by the CM induction of apoptosis. It is an example of anti-CD7 scFv immunotoxin CC method for producing the fusion protein, and a vaccine comprising the CM fusion protein is used in the treatment CM disorders involved a hyperproliferation of CD7-positive cells, a CM especially acute T-cell and/or myeloid leukaemia, and also in the CM conditioning an animal (e.g. a human) to be transplanted with donor CM conditioning an animal (e.g. a human) to be transplanted with donor CM cells, tissue or organ comprises: (a) depleting the CD7-bearing cell condition in the animal; (b) providing a transplant comprising isolated bone marrow and/or stem cell-enriched peripheral blood cells of the CM condition or therapeutic composition comprising the fusion protein; and (c) introducing the transplant into the animal
                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 651 AA;
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CD7 antibody or its fragment and an immunotoxin, useful for treating CD7
positive acute T-cell and/or myeloid leukemias, or Graft-versus-host
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N-PSDB; ACF05481.
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                                                                                                                                                                                                                                                                                    Local Similarity
      77
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                                                                                                                                                     1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVXLLIFYSSNLHSGVPS
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RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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Search completed: December 23, 2004, 18:57:41 Job time: 30.8913 secs

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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US-09-652-559-3
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US-08-487-761-13
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US-08-458-516-5
US-08-649-100-17
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TTUSAC	SLPASIO         SLPASIO	100 100 tive	Cation US/0922 N: N: KENYA NOBUO AMA, MAMORU I, HIROMASA N: PROCESS FOR NUMBER: US/ FE: 199-01-0 NUMBER: US 08 1995-03-21 NUMBER: US 08 1995-03-21 NUMBER: US 08 1994-08-17 NUMBER: US 08 1991-09-17 NUMBER: US 08 1991-09-17 NUMBER: US 08 1991-09-18 VOS: 19 1991-09-18 VOS: 19 1991-09-18 VOS: 19 1991-09-18 VOS: 19 1991-09-18 VET: 2.0		107 107 107 107 127 127 127 127 214 214 214 214 214 214 214 214 214 214
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RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 	SLPASLGDRVTISCSASQDISNYLNWYQQKPD 	; Score 572; DB 4; L; Pred. No. 3.5e-51; 0; Mismatches 0;	3 55,322B 680 1133 178 178 774	ALIGNMENTS	US-08-146-206C-16 US-09-705-686-16 US-09-705-392A-16 US-09-705-392A-16 US-08-137-117D-37 US-08-137-117D-29 US-08-436-717-29 US-08-436-717-29 US-08-436-7137-29 US-08-436-7137-29 US-08-436-7137-29 US-08-437-642B-24 US-08-811-757-1 US-08-811-757-1 US-08-811-757-1 US-08-811-757-1 US-08-811-757-1 US-08-686-24 US-09-705-392A-24 PCT-US93-07332-24 US-08-403-853-18
TKLEIKR 108         KLEIKR 128	ODISNYLNWYQOKPDGTVKLLIFYSSNLHSGVPS 60	ength 128; Indels 0; Gaps 0,	CHIMERA ANTIBODY		Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 37, Appl Sequence 37, Appl Sequence 29, Appl Sequence 29, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 24, Appl

INFORMATION:

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APPLICANT: HANAI, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-01-05
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1994-09-17
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-09-17
EARLIER APPLICATION NUMBER: US 08/375
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: US 08/375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
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APPLICANT: HASEGAWA, MAMORU
APPLICANT: HYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT FILING DATE: 1995-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/202,178
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US 08/27,178
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: US 08/202,178
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: US 08/202,178
PRIOR PILING DATE: 1991-09-18
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Patent No. 649566
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Best Local (
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LENGTH: 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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APPLICANT: HANAI, NOBUO
APPLICANT: HASGAWA, MAMORU
APPLICANT: HASGAWA, MAMORU
APPLICANT: HASGAWA, MAMORU
APPLICANT: KUMANA, YOSHHHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER PILING DATE: 1995-03-21
EARLIER PILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1991-09-17
EARLIER FILING DATE: 1992-09-17
EARLIER FILING DATE: 1991-09-18
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; OTHER INFORMATION: cDNA KM-641
US-09-764-304-10
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Best Local S
Matches 108
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Best Local Similarity
Matches 108; Conserv
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Patent No. 6
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TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                       Local Similarity
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81
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  RESGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
                                                                                         DIOMTOTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
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ilarity 100.0%;
Conservative (
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Pred. No. 3.5e-51;
0; Mismatches 0;
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RESULT 5 US-09-065-059-3

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                                                                                                                                                                                                                                                              Sequence 35, Application US/08652558 Patent No. 5861155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.2%;
Best Local Similarity 89.8%;
Matches 97; Conservative
                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/065,0 FILING DATE: CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Bucca Ph.D., Danidel REGISTRATION NUMBER: P-42,368 REFERENCE/DOCKET NUMBER: 50356-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                    APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                 NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 108 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
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                                                        COUNTRY:
                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
                                                                                              BOSTON
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                                                                          MASSACHUSETTS
                                                                                                           B: BANNER & WITCOFF
75 STATE STREET, 23RD FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: McDermott, Will & Emery 99 Canal Center Plaza
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                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THERAPEUTIC AGENT FOR HEPATITIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08236520 Patent No. 5591629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 96; Conserv
                                                                     APPLICATION NUMBER: US/08/234
FILING DATE: 29-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MMV!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    STREET: Law CITY: Lexington CITY: Massachusetts
                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/IB94/0 FILING DATE: NOVEMBER 21, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rodriguez, Mos
APPLICANT: Miller, David
TITLE OF INVENTION: MONOC
TITLE OF INVENTION: CENTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: YANKWICH, LEON R. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C STREET: Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RPSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPRTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez, Moses
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                                                           617-861-6240
                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MONOCLONAL ANTIBODIES WHICH PROMOTE CENTRAL NERVOUS SYSTEM REMYELINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
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                                                                                               MMV92-01
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Pred. No. 3.2e-44;
5; Mismatches 6
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; MOLECULE TYPE: protein
PCT-US95-05262-2
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PCT-US95-05262-2
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                                                                                                                                       Query Match
Best Local Similarity
Matches 96; Conserv
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Best Local Similarity
Matches 96; Conserv
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STREET: Lexington
CITY: Lexington
CTATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: April 29, 1:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mayo Foundation for Medical Education Research TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/05262 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C STREET: Two Militia Drive
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 81
                    61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
                                                                                  1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
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amino acid
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3Y: linear
RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 128
                                                                                                                                     87.8%; ilarity 88.9%; Conservative
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29, 1994
                                                                                                                                     Score 502; DB 5;
Pred. No. 5.2e-44;
3; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                           MMV92-01 PCT
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                                                                                                                                         9;
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                                                                                                                                       Indels
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US-08-487-761-13
RESULT 10
US-09-386-658A-4
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Patent No. 6217866
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/487,761
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,411
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: GOODERS POSSERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215) 454-3808 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cheadle, Christoph
APPLICANT: South, Victoria J.
TITLE OF INVENTION: Monoclona
TITLE OF INVENTION: Epidermal
TITLE OF INVENTION: Employing
                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: GOOdman, ROBANNE
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Macintosh
OPERATING SYSTEM: SYSTE
SOFTWARE: Word 5.0 (Pai
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (215) 454-3808
                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                     61 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKIPYTFTGGTKLEIKR 108
                                                                                                                                                                                                              94;
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                                                                                                                                          EIHMTQTTSSLSASLGDRVTISCSASQDIRNYLNWYQQKPDGTVKLLIYYTSTLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Kris, Richard
                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                          87.1%;
87.0%;
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Epidermal Growth Factor Receptor and Therapeutic Methods
Employing Same
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                                                                                                                                                                                                          Score 498; DB 3;
Pred. No. 1.1e-43;
6; Mismatches 8
                                                                                                                                                                                                                                            DB 3; Length 112;
                                                                                                                                                                                                              Indels
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Sequence 4, Application US/09386658A
Patent No. 6593137
GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard F.
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575/54182

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                                                           Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 93; Conser
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                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/386,658A CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Co, Man Sung
APPLICANT: TBO, J. Yun
TITLE OF INVENTION: GPIIB/IIIA
TITLE OF INVENTION: GPIIB/IIIA
                                                                                                                                                                   LENGTH: 107 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One manager CITY: San Francisco
                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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                                                                            Similarity
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DIQMTQTASSLEASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
                                                                                                                                                    TYPE: protein
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                                                                         85.3%;
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86.1%;
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                                                       Score 488; DB 1; Length 107; Pred. No. 1.1e-42; 4; Mismatches 10; Indels
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Pred. No. 1.3e-43;
8; Mismatches 7
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US-08-649-100-17
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US-08-458-516-5
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APPLICANT: Co, Man Sung
APPLICANT: TSo, J. Yun
TITLE OF INVENTION: Human
TITLE OF INVENTION: GPIIE
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                      Matches
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Patent No. !
                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
RAPPLICATION UNUMBER: US 08/
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORWATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSES: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                     ocal Similarity
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                                                                                          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
                                                                                                                                             21 DIOMTOTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGIVKLLIYYTSTLHSGVPS
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                                                                                                                                                                                                                Score 488; DB 1;
Pred. No. 1.3e-42;
4; Mismatches 10
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                                                                                                                                                                                                                      10; Indels
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; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAI
; APPLICANT: MATUSUE
; APPLICANT: NAGATA,

SHIRAKAWA, KAMON MATUSUE, TOMOKAZU NAGATA, SHIGEKAZU

APPLICANT:

Sequence 17, Application US/08649100 Patent No. 6114507

APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

41

STREET: PO BOX 747 CITY: FALLS CHURCH

E: BIRCH, STEWART, KOLASCH AND BIRCH

۷A

ADDRESSEE:

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Sequence 7, Application US/09199149

Fatent No. 6150099

GENERAL INFORMATION:

APPLICANT: Jonak, Zdenka L.

APPLICANT: Taylor, Alexander H.

APPLICANT: Trulli Jr., Stephen H.

APPLICANT: Johanson, Kyung O.

ITILE OF INVENTION: Humanized Monoclonal Antibodies

FILE REFERENCE: P50860

CURRENT APPLICATION NUMBER: US/09/199,149

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

LENGTH: 108
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                                                                            ; TYPE: PRT ; ORGANISM: murine cells US-09-199-149-7
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Best Local S
Matches 94
 Query Match
Best Local Similarity
Matches 92; Conserv
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FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELBEAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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 85.1%; ilarity 85.2%; Conservative
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Score 487; DB 3; Length 108; Pred. No. 1.4e-42; 6; Mismatches 10; Indels
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APPLICANT: Bajorath, Jurgen
APPLICANT: Fell, H. Perry
APPLICANT: Fell, H. Perry
APPLICANT: Fell, H. Perry
APPLICANT: Felliland, Lisa K.
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BIOLOGICALLY ACTIVE BISPECIFIC
TITLE OF INVENTION: FUSION PROTEINS IN AMMALIAN CELL
FILE REFERENCE: 30436.18USD2
CURRENT FAPLICATION NUMBER: US/09/813,659
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 09/549,067
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 1995-10-05
PRIOR FILING DATE: 1995-10-05
PRIOR FILING DATE: 1995-09-13
PRIOR FILING DATE: 1993-09-13
PRIOR FILING DATE: 1993-09-13
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US-09-813-659-30
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Search completed: December 23, Job time: 8.13276 secs
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; SEQ ID NO 30
; SEQ TO NO 30
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 92; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Ledbetter, Jeffrey
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 32
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                                                                                                          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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                                                                        RFSGSGSGTDYSLTIANLQPEDIATYFCQQGNTLPWTFGGGTKLVTKR
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85.2%;
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                 2004, 19:08:02
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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n2_6/ptodata/2/pubpaa/USOB_NEW_PUB.Dep:*
n2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
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gn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
SUMMARIES
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DB ID  9 US-09-764-304-10 9 US-09-764-304-19 9 US-09-764-304-19 14 US-10-265-713-19 14 US-10-166-626-10 14 US-10-166-626-19 19 US-09-056-160B-10 14 US-10-164-671-10 14 US-10-197-080-4 17 US-10-741-657A-16 17 US-10-741-657A-16	107	107	109	131	131	108	108	128	128	128	128	128	128	Length
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127	107	107	107	107	585	504	302	302	302	302	274	274	108	657	656	643	642	638	637	601	127	108	107	107	107	107	107	107	107	107	107
14	14	14	15	14	15	14	14	14	9	9	14	9	14	16	16	16	16	16	16	9	14	13	16	16	16	16	16	15	15	15	15
US-10-268-883-5	US-10-268-883-6	0-269-010-	US-10-389-679-10	-10-310-674A-	US-10-107-991B-3	207-655-3	283-610A-	-10-2	US-09-813-659-32	US-09-813-659-18	US-10-283-610A-30	US-09-813-659-30	US-10-141-908-7	US-10-296-085A-68	US-10-296-085A-39	-10-296-085A-6	-10-296-085A-3		'n	US-09-480-236-1	US-10-084-139-2	-10-140-5	-10-410-913-	-10-287-994-	US-10-411-012-52	-10-410-997-5	US-10-410-930-52	49-	US-10-410-962-52	US-10-411-026-52	US-10-411-037-52
<u>ს</u>	Sequence 6, Appli	, '	10,	34	u ۲	348	32,	e 18,	32,	,	e 30,	ŏ,	7,	68,	39,	Sequence 69, Appl	38,	21,	e 16	,-	ν,	4	52,	e 52,	о 5	52,	52,	52,	o o	e 52,	Sequence 52, Appl

## ALIGNMENTS

US-09-764-304-10

Sequence 10, Application US/09764304

Patent No. US2002026036A1

GENERAL INFORMATION:

APPLICANT: HAMAI, NOBUO
APPLICANT: HAMAI, NOBUO
APPLICANT: HAMAI, NOBUO
APPLICANT: HIYAJI, HIROMASA
APPLICANT: HIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT PILING DATE: 2001-01-19
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER PILING DATE: 1995-09-17
EARLIER APPLICATION NUMBER: US 08/408,133

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Sequence 10, Application US/10265713
Publication No. US20030095964A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAAI, HIROMASA
APPLICANT: MIYAAI, HIROMASA
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OTHER INFORMATION: light chain
OTHER INFORMATION: variable region
US-09-764-304-19
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CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US 08/292,178
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Best Local Similarity
Matches 108; Conserv
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SEQ ID NO 19
LENGTH: 128
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Best Local Similarity
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APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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                                                                                                                                                                                                                                                                                                                                         DIOMTOTASSLEASIGDRVTISCSASODISNYLNWYQQKEDGTVKLLIFYSSNIHSGVES
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APPLICANT: MIYAII, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/265,713
CURRENT FILING DATE: 1999-01-05
PRIOR PILING DATE: 1999-01-05
PRIOR PILING DATE: 1995-05-31
PRIOR PILING DATE: 1995-05-31
PRIOR PILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1991-09-18
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SEQ ID NO 10
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEBTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 19, Application Us, publication No. US2003009599; GENERAL INFORMATION: GENERAL ENTARA, KENYA APPLICANT: HANAI, NOBUO APPLICANT: HASEGAWA, MAMOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT APPLICATION NUMBER: US/09/225,322
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR PELICATION NUMBER: US 08/454,680
PRIOR PILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR PILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR PILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR PILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: US07/947,674
                                                                                           SOPTWARE: PatentIn Ver. 2.0
SQ ID NO 19
SQ IENGTH: 128
TYPE: PRT
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Best Local
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                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19
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                             ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:light chain
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HASEGAWA, MAMORU
MIYAJI, HIROMASA
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No. US20030095964A1
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7.18

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APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NAMORU
APPLICANT: KUWANA, MAMORU
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR APPLICATION NUMBER: US/09/25,322B
PRIOR APPLICATION NUMBER: US/09/25,332B
PRIOR APPLICATION NUMBER: US/09/25,332B
PRIOR APPLICATION NUMBER: US/08/454,680
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                                                                                                                                               US-10-166-626-19
                                                                                                                                                                          RESULT 6
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                                                                      Sequence 19, Application US/10166626 Publication No. US20030166876A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10166626 Publication No. US20030166876A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 3-238375 PRIOR FILING DATE: 1991-09-18
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/292,178 PRIOR FILING DATE: 1994-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 108; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US07/947,674
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                                                                                                                                                                                                                                                                                            RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                           DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 572; DB 14; 100.0%; Pred. No. 3.5e-45;
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; OTHER INFORMATION: Description of Artificial Sequence:light chain ; OTHER INFORMATION: variable region US-10-166-626-19
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US-09-056-160B-10
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PRIOR FILING DATE: 1995-05-31
PRIOR PELICATION NUMBER: US 08/408,133
PRIOR PELING DATE: 1995-03-21
PRIOR FILING DATE: 1995-03-21
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1992-09-17
PRIOR PILING DATE: 1992-09-17
PRIOR PILING DATE: 1991-09-18
PRIOR PILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10,
Patent No. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 572; DB 14; Best Local Similarity 100.0%; Pred. No. 3.5e-45; Matches 10%; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
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TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 128
                                        APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
APPLICATION NUMBER: FILING DATE: 06-AUG
                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
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Lowman, Henry B.
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US-10-234-671-10
, Sequence 10, Application US/10234671
; Publication No. US20030190317A1
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                       INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hasak, Janet E.
REGISTAN NUMBER: 28,616
REFERENCION NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acids
TYPE: Amino Acid
TOPOLOGY: Linc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 61/054856
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 61/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cul, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: 91093R2C1
TELECOMMUNICATION: 650/225-8674
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTI-VEGF ANTIBODIES NUMBER OF SEQUENCES: 131
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                   LENGTH:
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Lowman, Henry B.
Chen, Yvonne M.
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amino acids
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Pred. No. 1.6e-39;
7; Mismatches 6
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US-08-779-784-21
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                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-779-784-21
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Best Local Similarity 88.0%;
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                                                                   Best Local
Matches 9
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JR4-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                   Query Match
                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rodriguez, Mos
APPLICANT: Miller, David
APPLICANT: Asakura, Kunih
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 119
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STREET: Floor
CITY: Hackensack
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ZIP: 07601
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 DIOMTOTTSSLSASLGDRVTISCRASODISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
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                                                                     Conservative
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                                                                                 87.8%;
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Pred. No. 1.6e-39;
7; Mismatches 6;
                                                                   Score 502; DB 8,
Pred. No. 1e-38;
3; Mismatches
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Continental Plaza, 4th
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; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mouse
US-10-197-080-4
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
                                                                                         NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn vers
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10197080 Publication No. US20030113940A1
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Best Local Similarity
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Publication No. US20030185827A1
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                                                                                                                                                                    APPLICANT: Erlanger, Bernard F.
APPLICANT: Sheetz, Michael
APPLICANT: Sheetz, Michael
APPLICANT: Sheetz, Michael
APPLICANT: Brus, Louis
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NANOTUBES AND RELATED METHODS AND COMPOSIFILE REFERENCE: 0575/67096-A
CURRENT APPLICATION NUMBER: US/10/197,080
CURRENT FILING DATE: 2002-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
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                                                                                                                        version 3.1
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Pred. No. 1e-38;
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; NAME/KEY: DOMAIN
; LOCATION: (1)..(107)
US-10-473-977-69
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US-10-473-977-69
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US-10-741-657A-16
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TITLE OF INVENTION: ANTIBOLIES AGAINST GPR64 AND USES THEREOF
FILE REFERENCE: 05882.0177.NPUS01
CURRENT APPLICATION NUMBER: US/10/741,657A
CURRENT FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 16
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Query Match 85.8%;
Best Local Similarity 87.9%;
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 69
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Best Local Similarity
Matches 94; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MATEO DE ACOSTA DEL RIO, Cristina M. et al TITLE OF INVENTION: GANGLIOSIDE-ASSOCIATED RECOMBINANT ANTIBODIES AND TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMORS FILE REFERENCE: 4565-0107P (US) 10/473,977.
CURRENT FILING DATE: 2003-10-03 PRIOR APPLICATION NUMBER: US/10/473,977.
CURRENT FILING DATE: 2003-10-03 PRIOR APPLICATION NUMBER: PCT/CU02/00003 PRIOR APPLICATION NUMBER: PCT/CU02/00003 PRIOR FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: CU 84/2001 PRIOR FILING DATE: 2001-04-06 PRIOR FILING DATE: 2001-04-06 PRIOR FILING DATE: 2001-04-06 PRIOR FILING DATE: 2001-04-06 PRIOR PRIOR SECULATION NUMBER: CU 84/2001 PRIOR FILING DATE: 2001-04-06 PRIOR PRIO
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TYPE: PRT
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87.9%; Pred. No. 4.6e-38;
tive 3; Mismatches 10;
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Score 491; DB 17;
Pred. No. 8.8e-38;
3; Mismatches 10;
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Pred. No. 2.5e-38;
8; Mismatches 7;
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; ORGANISM: Mus musculus
US-10-411-037-52
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PRIOR FILING DATE: 2001-10-10
PRIOR PELICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR PILING DATE: 2002-07-17
                                                                                                                  GENERAL INFORMATION:
                                                                                                                                  Sequence 52, Application US/10411026 Publication No. US20040063911A1
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Best Local
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SEQ ID NO 52
LENGTH: 107
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                                                      APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/411,037 CURRENT FILING DATE: 2003-04-09
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APPLICANT: DeFrees, Shawn
APPLICANT:
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NUMBER OF SEQ ID NOS: 75
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Bowe, Caryn
              Bayer, Robert
Hakes, David
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Pred. No. 1.7e-37;
4; Mismatches 10;
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; TYPE: PRT ; ORGANISM: Mus musculus US-10-411-026-52
Search completed: December 23, 2004, 19:35:50 Job time : 26.5684 secs
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PRIOR FILLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILLING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILLING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILLING DATE: 2002-06-25
PRIOR PILLING DATE: 2002-07-17
PRIOR FILLING DATE: 2002-07-17
PRIOR FILLING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILLING DATE: 2002-08-16
PRIOR FILLING DATE: 2002-08-28
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Best Local
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CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
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                                                                                             RESGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIK 107
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Pred. No. 1.7e-37;
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Gapop 10.0 , Gapext 0.5
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  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Db 4 bvowirgTrssLsasigDRVTTisCsAskggisNY  Oy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYS	A;Residues; 1-111 <ruf> A;Cross-references: UNIPROT:Q91WS9 C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;19-93/Domain: immunoglobulin homology <imm> Cuery Match Best Local Similarity 88.9%; Score 520; DB 2; Le Best Local Similarity 88.9%; Pred. No. 1.1e-40; Matches 96; Conservative 7; Mismatches 5; Matches 100MTQTASSLPASIGDRVTISCSASQDISNYLNWYQQKPI Cy 1 [[                                  </imm></ruf>	RESULT 1  A38740  Ig kappa chain V region (Py20) - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Oct-1991 #sequence_revision C;Accession: A38740  R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Biol. Chem. 266, 6607-6613, 1991  A;Tile: Heavy and light chain variable A;Reference number: A38740; MUID:911779  A;Status: preliminary; nucleic acid seq A;Molecule type: mRNA	30 466 81.5 105 2 PH0087 31 462 80.8 107 2 C48677 32 461 80.6 108 2 S11124 33 447 78.1 108 2 B30551 34 429 75.0 115 2 A53276 35 426 74.5 108 2 S38564 36 421 73.6 93 2 S38564 37 419 73.3 129 2 S52789 38 408 71.3 129 2 S40367 40 402 70.3 108 2 S40367 41 402 70.3 108 2 S44014 42 400 69.9 108 1 K1HURY 43 399 69.8 108 1 K1HURY 44 399 69.8 108 1 K1HURY 45 396 69.2 108 2 S19674 ALIGNMENTS
C;Accession: E38740  R;Ruff-Jamison, S.; Campos-Go)  J. Biol. Chem. 266, 6607-6613  A;Title: Heavy and light chail  A;Reference number: A38740; M  A;Accession: E38740  A;Status: perliminary; nuclei  A;Molecule type: mENA  A;Residues: 1-111 <ruf> A;Cross-references: UNIPROT:O</ruf>	61  SULT 2  8740  Rappa chain species: Mus pate: 18-Oct Accession: E accession: E accession: E status: prel molecule type Residues: 1-Cross-refere conversed to the substantial substantia	A;Residues: 1-11 cRU A;Cross-references: U C;Superfamily: immuno C;Keywords: heterotet F;19-93/Domain: immun Query Match Best Local Similari Matches 96; Cons Qy 1 DIQWTQT Qy 61 RFSGSGS Qy 1 DIQWTQT Qy 1 DIQWTQT C,Species: Mus muscul C;Species: Mus muscul C;Species: Mus muscul C;Accession: E38740 R;Ruff-Jamison, S.; C J: Biol. Chem. 266, 6 A;Tatle: Heavy and li A;Reference number: A A;Accession: E38740 A;Status: preliminary A;Nolecule type: mRNA A;Residues: 1-11 cRU A;Cross-references: U C,Superfamily: (ampur) A;Cross-references: U C,Superfamily: (ampur) A;Cross-references: U C,Superfamily: (ampur) A;Cross-references: U C,Superfamily: (ampur) A;Cross-references: U	RESULT 1  A38740  A38740  Ig kappa chain V regices: Mus muscul C; Species: Mus muscul C; Accession: A38740  R; Ruff-Jamison, S.; C; Biol. Chem. 266, 6  A; Rifle: Heavy and li A; Reference number: A A; Accession: A38740  A; Residues: preliminary A; Molecule type: mRNA A; Residues: 1-111 < RU C; Cysperfamily: immuno C; Keywords: heteroctet F; 19-93/Domain: immun C; Keywords: heteroctet F; 19-93/Domain: immun C; Reywords: heteroctet F; 19-93/Domain: heteroctet F; 19-93/
	Db 4 DVQMTQTTSSLSASLGDRVTTSCSAS  Qy 61 RFSGGGSGTDYSLTISNLEPEDIATY	A;Residues: 1-111 < RUF> A;Residues: 1-111 < RUF> A;Cross-references: UNIPROT:Q91WS9 C;Superfamily: immunoglobulin V region; C;Keywords: heterotetramer; immunoglobu F;19-93/Domain: immunoglobulin homology Query Match Best Local Similarity 88.9%; Pred. Hest Local Similarity 89.9%; Pred. Hest Local Similarity 99.9%; Pred. Hest Loca	RESULT 1 A38740 Ig kappa chain V region (Py20) - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_chang C;Accession: A38740 R;Ruff-Jamison, S; Campos-Gonzalez, R.; Glenney Jr., J.R. J. Biol. Chem. 266, 6607-6613, 1991 A;Title: Heavy and light chain variable region sequences and a A;Reference number: A38740; MUID:91177923; PMID:1706720 A;Accession: A38740 A;Residues: preliminary; nucleic acid sequence not shown; not co A;Accession: Heavy and light chain variable region sequences and a A;Residues: 1-11 < RUF> A;Cross-references: UNIFROT:091WS9 C;Superfamily: immunoglobulin v region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin F;19-93/Domain: immunoglobulin homology < IMM> Ouery Match Best Local Similarity 88.9%; Pred. No. 1.1e-40; Matches 96; Conservative 7; Mismatches 5; Indels Ouery Match A DVQMTQTTSSLSASLGDRVTISCSASQDISNYLNWYQQKPDGTVXLLI ON A DVQMTQTTSSLSASLGDRVTISCSASQDISNYLNWYQQKPDGTVXLLI ON A RFSGSGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTXLEIKR ON A RFSGSGSGTDYSLTISNLEPEDIATYFCHQYSKUPWTFGGGTKLEIKR ON A RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKVPWTFGGGTKLEIKR C;Species: Mus musculus (house mouse)

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Ig kappa chain v region, once mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49026; PL0220
C;Accession: B49026; PL0220
R;Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.
R;Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.
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A;Residues: 1-107 <PUC>
A;Experimental source: strain lupus-prone MRL-lpr/lpr mouse C;Superfamily: immunoglobulin V region; immunoglobulin homo C;Keywords: heterotetramer; immunoglobulin E;16-90/Domain: immunoglobulin homology <IMN>
F;24-34/Region: complementarity-determining 1
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A;Note: sequence extracted from NCBI backbone (NCBIP:60876)
R;Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz
J. Exp. Med. 171, 1919-1930, 1990
A;Title: An immunoglobulin 1916 tohain from a lupus-prone mu A;Reference number: PL0220; MUID:90278348; PMID:1893654
A;Accession: PL0220
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C;Superfamily: immunoglobulin V region; immun
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>
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A; Title: Molecular heterogeneity of auto-anti-idiotypic A; Reference number: A49026; MUID:91364791; PMID:1909645
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Ig kappa chain V region (Py69) - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C;Bpecies: Mus musculus (house mouse) (C;Date: 18:Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004 C;Accession: G38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Biol. Chem. 266, 6607-6613, 1991
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: G38740
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A;Title: B-cell proliferation initiated by Ia cross-linkin A;Reference number: S69900; MUID:92165291; PMID:1537587
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA
A;Residues: 1-108 <WY3>
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A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region;
                                                           A; Molecule type: mRNA
                                                                              A, Status: preliminary; nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.6e-39;
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Pred. No. 4.7e-39;
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PMID:1537587
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RyChen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nuclectide and translated amino acid sequences of cDNA coding f A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: A29380
A;Molecule type: mRNA
A;Residues: 1-122 CCHE>
A;Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1;
A;Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1;
A;Note: the authors translated the codon TTC for residue 1 as Leu C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross references: UNIPROT:P01643
C;Comment: This chain was isolated from a myeloma protein.
C;Comment: An immunoglobulin heterotetramer subunit consists of two identical c;Complex: An immunoglobulin becases, such as IgA and IgM, the subunits associal cisuperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
A29380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Determination of the primary structure of a mouse IgG2a A;Reference number: A01926; MUID:76091934; PMID:812696 A;Accession: A01926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A01926
R;Schiff, C.; Fougereau, M.
Eur. J. Biochem. 59, 525-537, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V region (MOPC 173) - more considered to the mouse (Species: Mus musculus (house mouse) C;Date: 24-Apr-1984 #sequence_revision
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                                                                                                                                                                                                                                                                                                    Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_chang
C;Accession: A29380
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Pred. No. 4.9e-39;
7; Mismatches 7;
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Pred. No. 1.1e-38;
                 Score 495; DB 2;
Pred. No. 2.4e-38;
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R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-li A;Reference number: S69900; MUID:92165291; PMID:153758
           r;22-96/Domain: immunoglobulin homology <IMM>
r;30-40/Region: complementarity-determining
                                                                                               A;Cross-references: GB:M27793; NID:g197161; PIDN:AAA38937.1; PID A;NOte: the authors translated the codon AGG for residue 30 as Statement of the codon AGG for residue 30 as Statement of the codon AGG for residue 30 as Statement of the codon AGG for residue 30 as Statement of the codon AGG for residue 30 as Statement of the codon AGG for residue 30 as Statement of the codon AGG for residue 31 as Aguarda a
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R;Kaartinen, M.; Rocca-Serra, J.; Mackelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene
A;Reference number: JL0076; MUID:89096973; PMID:3211160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain precursor V region (anti-phenyloxazolone, 18C10) C;Species: Mus musculus (house mouse) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change C;Accession: JL0080
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A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY2>
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C;Accession: 869903; 869904; 869905
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A;Residues: 1-115 <KAA>
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                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JL0080
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complementarity-determining complementarity-determining
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Pred. No. 3.1e-38;
4; Mismatches 9
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PMID:1537587
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18 Ser
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A; Accession: PH0888
A; Molecule type: mRNA
A; Residues: 1-109 <SHA>
C; Superfamily: immunoglobulin V region;
C; Keywords: immunoglobulin homology
F; 16-90/Domain: immunoglobulin homology
                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision(
C;Accession: PHO888
R;Shalaby, M.R.; Shepard, H.M.; Presta,
J. Exp. Med. 175, 217-225, 1992
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C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul
C;Accession: A01927
R;Siegelman, M.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981
A;Title: Complete amino acid sequence of light chain variable regions A;Reference number: A01927; MUID:82150934; PMID:6801658
A;Accession: A01927
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PH0888
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A;Experimental source: strain A/J
A;Note: hp 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr,
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                 Query Match
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                 85.3%;
Score 488; DB z; r
Pred. No. 9.1e-38;
No matches 11;
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Pred. No. 7.3e-38;
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Pred. No. 3.4e-38;
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                                                                                          immunoglobulin homology
                                                              <IMM>
                                                                                                                                                                                               Rodrigues, M.L.; Beverley, P.C.L.;
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Ig kappa chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Ju
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Ju
C;Accession: A34904
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idic
A;Feference number: A34903; MUID:90094387; PMID:2104617
A;Accession: A34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-126 <BED>
A;Cross-references: UNIPROT:091WF8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-109/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region - mouse
c;Species: Mus musculus (house mouse)
c;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S38862
C;Accession: S38862
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
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S38862
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A34904
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A;Molecule type: mRNA
A;Residues: 1-108 <FIS>
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                   RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKL-PWTFGGGTKLEIK 107
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                                                                           DVQMTQTTSSLAASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
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Pred. No. 1.5e-37;
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Pred. No. 1.1e-37;
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Listing first 45 s
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KV5G MOUSE
Q6GMX9
Q6GMX9
Q6GMXN
KV1R HUMAN
Q6GMM1
KV1L HUMAN
Q7Z3Ÿ4
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KVSU MOUSE
AAR11052
AAR11043
AAR11040
KV1B HUMAN
KV1O HUMAN
KV1Y HUMAN
KV1A HUMAN
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KV1A HUMAN
OSUL70
O96SA9
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KV5J MOUSE
KV5K MOUSE
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AAR10992
KV5N MOUSE
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P01594 homo sapien P01607 homo sapien P0362 homo sapien P01593 homo sapien P01593 homo sapien Q9u170 homo sapien Q9u177 homo sapien Q9u177 homo sapien P01639 mus musculu Q6gmx9 homo sapien P01610 homo sapien P01610 homo sapien P01610 homo sapien P01604 homo sapien Q7z3y4 homo sapien Q7z3y4 homo sapien Q7z3y4 homo sapien P01605 homo sapien
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   RP SEQUENCE FROM N.A.

RP CSTRAIN=YVB/N, TISSUE-Colon;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altachul S.F., Zeebbarg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altachul S.F., Zeebbarg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Wass S.I., Wang J., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Barownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Richards S., Worley A.C., Sodergran E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Mazna J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Mczywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.A.;

Jones S.J., Marra M.A.;

ROGIET S. W. Schmutz J., Wyers R.M., Schein J.E.,

RA Krzywinski M.A.;

ROGIET S. W. Schmutz J., Wyers R.M., Schein J.E.,

RA Krzywinski M.A.;

ROGIET S. W. Schmutz J., Wyers R.M., Schein J.E.,

RA Krzywinski M.A.;

RA
EMBL; BC013496; AAH13496.1; -.
PIR; A38740; A38740.
PIR; C38740; C38740.
PIR; B38740; G38740.
PIR; B38740; G38740.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_MCC.
InterPro; IPR003596; Ig_WCC.
Pfam; PF007554; C1-8et; 1.
Pfam; PF00047; ig; 1.
SMART; SM00406; IG_LIKE; 2.
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Submitted (
EMBL; BC013
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Q91WS9;
Q101-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID=10090; [1]
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
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QGGMXB
RVSP MOUSE
Q96PF6
Q96PF7
Q6P171
AH33111
KV1C HUMAN
KV1S HUMAN
Q9ULB1
KV1H HUMAN
Q7TS98
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Q6gmx8 homo sapien
P01649 mus musculu
Q96pf6 homo sapien
Q6pih7 homo sapien
Aah34141 homo sapien
P01595 homo sapien
P01616 homo sapien
P04431 homo sapien
P04431 homo sapien
P04431 homo sapien
P04603 homo sapien
P01600 homo sapien
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Database

Sequence: Title: Perfect score:

Scoring table:

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 Q8R062
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DOMAIN
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Im
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
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Hypothetical protein.
NON TER 1 1
SEQÜENCE 233 AA; 25781 MW; B1C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                      PIR; A01926; KVMS73.
HSSP; P01594; 1JV5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                              DOMAIN
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-I- MISCELLANEOUS: This chain was isolated
                                                                                                                                                                                                                                                                                                                                                                                                  Schiff C.,
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=76091934; PubMed=812696;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kappa chain
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                                                                                                                                          Similarity
                                                RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWIFGGGTKLEIKR
                                                                                      DIQMIQTISSLGASLGDRVTISCGASQSIGNYLBWYQQKPDGTVKLLIYYTSSLHSGVPS
                                                                                                  DIQMTQTASSLFASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
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                                                                                                                                Conservative
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Rodentia;
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85.2%;
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                                                                                                                                9;
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By similarity.
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Complementarity-determining-3.
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Complementarity-determining-2.
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Pred. No. :
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 PRT;
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light chain.";
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KYSK MOUSE
ID KVSK MOUSE
AC P01644;
DT 21-JUL-1986
DT 21-JUL-2004
DE 19 kappa chai

STANDARD;

PRT;

108 8

Ig kappa chain

(Rel. 01, Created)
(Rel. 01, Last sequence up)
(Rel. 44, Last annotation)
ain V-V region HP R16.7.

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Bistantein M.J., Uddin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Historica S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Chee S. T. Marra M. A.
                                                                                                                                                                                                                                                                            Query Match
Best Local
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; 1.
Pfam; PF07047; ig; 1.
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"Generation and initial analysis of and mouse cDNA sequences.";
"And mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 234 AA; 25858 MW; 4EB08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2002) to the EMBL; BC027418; AAH27418.1; HSSP; P01594; 1JV5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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81
                                                             61
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                                      RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
                                                                                                                                                        DIQMIQTASSLFASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                                                                                                                           DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS
RFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFPFTFGSGTKLEIKR
                                                                                                                                                                                                                                                  Conservative
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TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                             25858 MW; 4EB08C81426AEAB1 CRC64;
                                                                                                                                                                                                                                                                            86.4%;
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Last annotation updat
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                                                                                                                                                                                                                                               Score 494; DB 2; I
Pred. No. 4.1e-42;
6; Mismatches 8;
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RESULT 5

KYSL MOUSE

ID KYSL MOUSE

AC P01645;

DT 21-JUL-1986

DT 21-JUL-1986

DT 15-JUL-2004

DE 19 kappa che

OS Mus masculue

OC Eukaryota; h

OC Mammalia; EN

OC Mammalia; EN

OC NCBI TaxID=

RN [1]

RY SEQUENCE.

RP SEQUENCE.

RR STRALN=A/J;

RX MEDLINE=821:

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RI Proc. Natl.

CC -1- MISCELL

DR HSSP; P0160

DR InterPro; I

DR Pfam; PF000

DR SMART; SM00
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Best Local S
Matches 95
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HSSP; P01594; 1JV5.
InterPro; IPR007110;
InterPro; IPR003596;
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DISULFID
NON_TER
                                                                    MEDLINE-82150934; PubMed=6801658; Siegelman M., Capra J.D.; Siegelman M., Capra J.D.; Complete amino acid sequence of light chain variable from five monoclonal anti-p-azophenylarsonate antibodi with respect to a crossreactive idiotype."; Proc. Natl. Acad. Sci. U.S. A. 78:7679-7683(1981).
                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                    P01645;
21-JUL-1986 (Rel. 01, Created
21-JUL-1986 (Rel. 01, Last se
05-JUL-2004 (Rel. 44, Last an
Ig kappa chain V-V region HP
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DOMAIN
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"Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
-!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 1g; 1
SMART; SM00406; IGV;
             InterPro; IPR007110; Ig-like.
InterPro; IPR007596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA;
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50
57
98
108
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1 23 Framework-1.
24 34 Complementarity-determin
35 49 Framework-2.
50 56 Complementarity-determin
57 88 Framework-3.
89 97 Complementarity-determin
68 108 Framework-4.
23 88 By similarity.
                                                                                                                                                                                                                                                                                                                                                STANDARD;
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. 01, Last sequence 44, Last anno
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annotation update)
HP 93G7.
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.
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Pred. No. 5.4e-42;
}; Mismatches 10;
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RESULT 6
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ID AAR1
AC AAR1
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KV5N_MO

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Best Local
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Best Local (
KV5N MOUSE STANDARD; PRT; 108
P01647;
P01547;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upda
05-JUL-2004 (Rel. 44, Last annotation up
1g kappa chain V-V region HP 124E1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata;
Bukaryota; Metazoa; Rodentia; Sciurognat
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02-MAR-2004
02-MAR-2004
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NON TER
SEQUENCE
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Liang Z., Xie C., Chen C., Kre
"Antinuclear autoantibodies fr
Submitted (SEP-2003) to the EM
EMBL; AY436832; AAR10992.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR10992
AAR10992;
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DOMAIN
DOMAIN
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DOMAIN
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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MAR-2004 (TrEMBLrel. 27, Last sequence update)
MAR-2004 (TrEMBLrel. 27, Last annotation update)
immunoglobulin kappa light chain (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Rodentia;
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s from B6.Sle1 mice.
e EMBL/GenBank/DDBJ
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Pred. No. 6.9e-42;
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 Craniata; Vertebrata; Eutel
Sciurognathi; Muridae; Muri
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Matches 94
SMART; SM00406; ÎGV; 1.
PROSITE; PS50835; IG LIKE; 1
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DOMAIN 1 23
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DOMAIN 35 49
DOMAIN 50 56
DOMAIN 57 88
DOMAIN 89 97
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DOMAIN 98 108
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-V region HP 123E6.
Mus musculus (Mouse)
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                                                                                                                       "Complete amino acid sequence of light chain variable rec
from five monoclonal anti-p-azophenylarsonate antibodies
with respect to a crossreactive idiotype.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
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Mammalia; Eutheria;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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STRAIN=A/J;
STRAIN=A/J;
MEDLINE=82150934; PubMed=6801658;
Siegelman M., Capra J.D.;
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STRAIN=A/J;
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Rodentia;
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                      Immunoglobulin V region
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Pred. No. 1.8e-41;
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          Complementarity-determining-1
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Ig kappa chain V-V
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Direct protein sequencing;
                                                                                                                                                                                                                                                                              with respect to a crossreactive idiotype."; Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
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STRAIN=A/J;
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Mammalia; Eutheria;
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InterPro; IPR003596; Ig_v.
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                                                                                83.4%;
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87.0%;
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Immunoglobulin V region
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Pred. No. 9.
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Complementarity-determining-3.
Framework-4.
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                                                                                                            D52EDA5E9A45291C
                                                                                                                              similarity.
                                                                        Mismatches
                                                                                                                                                                                                                                                                    hybridoma
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                                                                                DB 1;
.1e-41;
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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X Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,

X Klausner R.D., Collins F.S., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L., Scheetz T.E.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L., Scheetz T.E.,

X Hopkins R.F., Jordan H., Fonaldo M.F., Carninci P., Prange C.,

X Hand S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Villalon E., Ketteman M., Madan A., Gylins S., Sanchez A.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Hones S. I. Maxis M., Salska U., Smailus D.E., Schnerch A., Schein J.E.,

X Jones S. I. Maxis M. A.
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                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF07654; C1-8et; 1.
Pfam; PF07047; 1g; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                Hypothetical
SEQUENCE 2
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STRAIN=FVB/N; TISSUE=Colon;
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STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC015292; AAH15292.1;
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terPro; IPR007110; Ig-like.

terPro; IPR003597; Ig-MC.

terPro; IPR003596; Ig-MC.

terPro; IPR003596; Ribosomal_S2.
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81
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                                                                                                                                                                                                                                                            Similarity
                                                                                                                                             DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS
                              RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR
RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVKR
                                                                                                            DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (TremBirel. 19,
1 (TremBirel. 19,
4 (TremBirel. 26,
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Last sequence up
Last annotation
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                                                                                                                                                                                                                              Score 466; DB
Pred. No. 2.9e
6; Mismatches
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9e-39;
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                                                         108
128
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RESULT 12
KVSU MOUSE
ID KVSU MOUSE
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DT 13-AUG-1987 (
DT 29-MAR-2004 (
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Best Local S
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JL84;
Q9JL84;
Q1-OCT-2
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NON TER
SEQUENCE
                             This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                           MEDLINE-83271467; PubMed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Mil
ManNA sequences define an unusually restricted
phenyloxazolone and its early diversification."
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infect. Immun. 68:5803-5808(2000).
EMBL; AF206022; AAF69320.1; -.
HSSP, P01594; 1JV5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20448942; PubMed=10992488; Malkiel S., Liao L., Cunningham M.W., I"T-Cell-dependent antibody response to
           modified
                                                                                                                                   Nature 304:320-324(1983).
-!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    streptococcal polysaccharide, with cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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-MAR-2004 (Rel. 43, Last annotation
kappa chain V-V region NQ5-89.4.
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87; Conserv
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7 (Rel. 05, Last
1 (Rel. 43, Last
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107 AA;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
immunoglobulin light chain variable region
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Rodentia;
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Rodentia;
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Ig_v.
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Pred. No. 4.9e-39;
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                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACF9B1253ACA1E5D CRC64;
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                                                                                         It is produced through
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co the dominant epitope
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                                              restrictions
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Best Local S
Matches 88
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Best Local S
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AAR11052;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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DOMAIN
                                                                                                                                                                                                                                                                                                                                            Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., "Antinuclear autoantibodies from B6.Slel mice."; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases EMBL; AY436892; AAR11052.1; -.
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=B6.Sle1; TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANA immunoglobulin kappa light chain
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ON_TER
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m; PP00047; ig; 1.

RT; SM00406; IGv; 1.

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ridoma; Immunoglobulin V r
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GSGSGTDYSLTISNLEEEDIATYFCQLGNTLPWTFGGGTKLE
                              GGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLE
                                                                                                                 MTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPSRFS
                                                                                       MTQTPSSLSASLGDRVT1SCRASQD1SYYLNWYQQKPDGTVKLL1YYTSRLHSGVPSRFS
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Framework-1.
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7; Mismatches
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By similarity.
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Sciurognathi; Muridae; Murinae;
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AAR11043;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation updat
ANA immunoglobulin kappa light chain (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=B6.Sle1; TISSUE=Spleen;
Liang Z., Xie C., Chen C., Kreska D., Hsu K.,
"Antinuclear autoantibodies from B6.Sle1 mice.
"Antinuclear autoantibodies from B6.Sle1 mice.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTPAIN-B6.Sle1; TISSUE-Spleen; Kre
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Mammalia; Eutheria;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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104 AA;
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from B6.Sle1 mice.
EMBL/GenBank/DDBJ
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ים אח, 1e-36;
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Pred. No. 1.3e-36;
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## ARBSULT 1 ARABATIS IID ARAB XX ARA ARC ARAB XX ARC XX ARC XX Gang XX Gang XX Gang XX Gang XX Cann XX C 30-SEP-1999; 99JP-00278291. 06-APR-2000; 2000JP-00105088. 29-SEP-2000; 2000WO-JP006774 05-APR-2001. Synthetic. cancer. Ganglioside; Ganglioside 03-JUL-2001 WPI; 2001-266143/27. Hanai WO200123432-A1. AAB81991; AAB81991 standard; protein; (КҮОМ ) КҮОМА НАККО КОСУО КК 'n Shitara K, GD3 GD3; complementarity determining region; (first entry) specific antibody related Nakamura 582 ζ, A Niwa protein SEQ CDR; antibody; 日 ĕ 57

Adn97489 Adm47075 Aar47453 Adm72029

Adn97491

Aae33522

Aae35327

The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification

Claim 39; Page 175-179; 183pp; Japanese.

New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

Aao31101 Aae33523 Adh34587 Abp58273 Abp58275

Query Match 100.0%; Score 3071; DB 4; Best Local Similarity 100.0%; Pred. No. 4.3e-149; Matches 582; Conservative 0; Mismatches 0;

Length

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06-APR-2000; 2000JP-00105088
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FFFXSXSSSSSXX
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Best Local Similarity
Matches 572; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 41; Page 168-172; 183pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 582 AA;
                                                                                                            LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                               STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                            TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                                                                   SVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
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Pred. No. 8.7e-147;
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GM2 antibody-related protein

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GM2; antibody; cytostatic; cytotoxic;

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Best Local Simi
Matches 523;
                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to derivatives of an antibody against ganglioside GM2. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK.
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                                                                                                                                                                                                                                                     GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                      SSGLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLSGLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
                                                                                                                                                                                                                                                                                               INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
                                                                     NNYKOPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISN
                                                                                                    RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGI
                                                                                                                                   DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                  YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                     DELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                         YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                        GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                             NNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNPHLRPRDLISN
                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 61-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura K,
                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 3.6
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3.6e-133;
nes 36;
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Query Match
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Matches 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant anti-EpCAM antibody having an amino acid sequence defining an immunoglobulin light or heavy chain framework region, for the diagnosis, prognosis and treatment of cancer.
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cancer; gene the
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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                   addfkgrfafsletststaflqinnlrsedtatyfcvrfiskgdy----wqqtsvtvss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.4%; Score 2744.5; DB 6; ilarity 88.5%; Pred. No. 2.1e-132; Conservative 31; Mismatches 31;
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Matches 515
                                                                                                                                                                            The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion proteins. The fusion protein comprises a non-interleukin-2 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is dI-KS-ala-IL2 (D20T) variant protein comprising dI-KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2 moiety, useful for preparing a composition for treating cancer, viral infections or immune disorders.
                                                                                                                                         Sequence 579
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12-APR-2002; 2002US-0371966P
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Unidentified
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                  Human type complementation-determining domain transplanted antibody and derivatives against ganglioside GD2, useful in diagnosis and therapy of e.g. tumors, has low antigenicity, little side effects but potent activity in cancer.
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30-SEP-1999;
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                                                                                                                                                                                                                                                              Ganglioside; GD2;
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                                                                                                                                                                                                                                                                                           specific antibody related protein SEQ ID NO:
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                              Nakamura
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Matches 518
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                                                                                                     immunoglobulin; variace cancer; cell surface
                       WO2004055056-A1
                                                                                                                                                             Humanised immunoglobulin heavy chain-IL-2
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                                                                                                   variable region; antibody; GD2; rface glycosphingolipid; IL-2.
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Pred. No. 9.7e-132;
4; Mismatches 39;
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                                                                                                                                                             protein SEQ ID NO:6.
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Query Match
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Matches 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified m14.18 antibodies with reduced immunogenicity specifically bind the human cell surface glycosphingolipid for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 517; Conserv
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DB; ADP42959.
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KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV
                                                                                    QGNVFSCSVMHEALHNHYTQKSLSLSFGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY
                                                                                                                                                TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                                                                                                                                      SVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGNVFSCSVMHEALHNHYTQKSLSLSPG-APTSSSTKKTQLQLEHLLLDLQMILNGINNY
                                                                                                                                                                                                                                      TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
                                                                                                                                                                                                                                                                                                                             SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.4%; Score 2715.5; DB 8 88.8%; Pred. No. 6.3e-131; tive 24; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; 51pp;
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                                                                                                                                                                        Matches 494;
                                                                                                                                                                                                                              The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion proteins. The fusion protein comprises a non-interleukin-2 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is Gl-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D2OT) variant protein comprising dI-KS heavy chain fused to human IL-2 (D2OT) variant protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                              Sequence 580 AA;
                                                                                                                                                                                                                                                                                                                             Example 10;
                                                                                                                                                                                                                                                                                                                                               New fusion protein comprising a non-IL-2 momoiety, useful for preparing a composition infections or immune disorders.
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12-APR-2002; 2002US-0371966P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dI-NHS76
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                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-513757/48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy;
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                 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFLGG
                           GLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVBPKSCDKTHTCPPCPAPELLGG
                                                        ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                  ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                            EVTLVESGGDFVKPGGSLKVSCAASGFAFSH-YAMSWVRQTPAKRLEWVAYISSGGSGTY
                                                                                                               YSDSVKGRFTISRDNAKNTLYLOMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS
                                                                                                                                   QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGS-TY
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (gamma4h)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin-2; IL-2; cancer; viral infection; immune disorder; apy; immunoglobulin; Ig; fusion protein; human; variant.
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                              Page 68-71;
                                                                                                                                                                                                                                                                                                                                                                                                                           LEXIGEN RES CENT CORP
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                                                                                                                                                                                 84.4%;
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                                                                                                                                                                                                                                                                                                                            71pp;
                                                                                                                                                                        31;
                                                                                                                                                                       Score 2592; DB 6;
Pred. No. 1.3e-124;
1; Mismatches 54;
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                                                                                                                                                                        54;
                                                                                                                                                                                        Length 580;
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RESULT 9
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                                      such fusion proteins. The fusion protein comprises a non-interleukin-2 (II-2) molety fused to a mutant II-2 molety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is dI-NNS76 (gammazh) (FN-AQ)-ala-II-2 (D20T) variant protein comprising dI-KS heavy chain fused to human II-2 (D20T) variant protein. This sequence is used to illustrate the method of the invention
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2001;
12-APR-2002;
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                                                                                                                                                                                            The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index
                                                                                                                                                                                                                                                             Claim 37;
                                                                                                                                                                                                                                                                                                      moiety, useful for pr
infections or immune
                                                                                                                                                                                                                                                                                                                          Move fusion protein comprising a non-IL-2 moiety fused to a mutant IL-moiety, useful for preparing a composition for treating cancer, viral
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (gamma2h)
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                                                                                                                                                                                                                                                           Page 64-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEXIGEN RES CENT CORP
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RESULT 10
AAO18400
ID AAO18
XX AAO18
AC AAO18
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CY 11-OC
XX MAUS
CKW MOUSE
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Best Local
                                    13-OCT-2000; 2000US-0240285P
13-MAR-2001; 2001US-0275289P
21-JUN-2001; 2001US-0299987P
                                                                                                                                                                                                                                                                      Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer; neoplasia; LT-beta-R; light chain; heavy chain; variable region.
                                                                                                                                                                                                                                                                                                                                   Mature
                                                                                                                                                                                    WO200230986-A2
                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO18400 standard;
                                                                                                            12-OCT-2001; 2001WO-US032140
                                                                                                                                                  18-APR-2002
     (BIOJ ) BIOGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WQQGNVFSCSVMHEALHNHYTQKSLSLSFGKAPTSSSTKKTQLQLEHLLLDLQMILNGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNPSLKSRVTISYDTSKNQFSLKLSSVTAADTAVYYCARGKWSK--FDYWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVTLVESGGDFVKPGGSLKVSCAASGFAFSH-YAMSWVRQTPAKRLEWVAYISSGGSGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI
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; Pred. No. 5.6e-123;
31; Mismatches 56;
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   15-APR-2004
                                                                                                                                                Artificial
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Query Match
Best Local Similarity
Matches 418; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanized anti-lymphotoxin-beta receptor antibody, useful for treating or reducing the advancement, severity or effects of neoplasia, particularly solid tumors (i.e. carcinomas) including colorectal cancer and breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 25-26; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-583337/62.
                                                                                                                                                                                                                                                                                                                                                          QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
                                                         LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                           LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                      STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                             PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                      GLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                     STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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Pred. No. 1.2e-105;
9; Mismatches 21;
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ADM97491
ID ADM97491 standard; protein; 713 AA.

XX
AC ADM97491;
XX
OT 01-JUL-2004 (first entry)
XX
DE Artificial protein construction protein #4.
XX
OE Artificial proprotein; propeptide; protein engineering; antibody.
XX
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
15-APR-2004.
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RESULT 12
ADN97489
ID ADN97
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AC ADN97
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DT 01-JU
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Best Local Simi
Matches 419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New artificial proprotein comprises three peptide sequences, useful artificial multimeric protein engineering in eukaryotes.
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             01-JUL-2004
                                      ADN97489;
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                                                              ADN97489
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DB; ADN97490.
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                                                                                                                                     TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                    LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                                    PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                                                                                                                                                                                      APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                            SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL----GTYYF---DSWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                            standard;
                                                                                                                                                                                                                                                                      APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                       PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
                                                                                                                                                                                                                                                                                                                                   PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
                                                                                                                                                                                                                                                                                                                                                                      ASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
                                                                                                                                                                                                                                                                                                                                                                                       TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
                                                                                                                                                                                                                                                                                                                                                                                                                   PDSVKGRFTISRDNDKNALYLOMNSLKSEDTAMYYCARRSEFYYYGNTYYYSAMDYWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTYTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   713 AA;
                                                                                                                      TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                       LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 64; 244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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             (first
                                                            protein;
             entry)
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                                                            715
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Pred.
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Mismatches
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                                                                                                                                               449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 713;
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                                   413
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                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                           419;
            TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide sequences: a first peptide sequence of interest, a propeptide sequence attached to the C-terminus of the first peptide sequence of interest, and a second peptide of interest attached to the C-terminus of the propeptide sequence. The artificial proprotein and polymucleotides are useful for artificial multimeric protein engineering, e.g. antibodies and antibody fragments in eukaryotes. This sequence corresponds to a protein used in the generation of the protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  artificial proprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New artificial proprotein comprises three peptide sequences, artificial multimeric protein engineering in eukaryotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002; 2002US-0415940P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Artificial protein construction protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an artificial proprotein comprising three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004031362-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LARG-) LARGE SCALE BIOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004-330170/30.
DB; ADN97488.
                                      PAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
                                                                                                                                                                                                                                                                                                                   TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
                                                                                                                                                                                                                                                                                                                                                                               SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL-----GTYYF---DSWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                              EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                              PDSVKGRFTISRDNDKNALYLOMNSLKSEDTAMYYCARRSEFYYYGNTYYYSAMDYWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      715 AA;
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                    PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                            PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                                                                                      APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                 PAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
                                                                                                                                                                                                                                                                                               ASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
                                                                                                                                                                                                                                                                                                                                                                                                                            EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTYTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2216;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                     858
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RESULT 13
ADM47075
ID ADM4777
XX ADM477
XX MOUSE
XX MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the production of a methylotroph yeast that produces mammalian sugar chains, comprising disrupting the OCH1 gene in the yeast that encodes for alpha-1,6-mannosyl transferase and inserting and expressing the alpha-1,2-mannosidase gene. The specification also includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase (URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase (AAE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-10 cisopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRE1); and (h) aspartic protease (YPS1), mannosyl transferase (KTR1 or MNN9), alcohol oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene sequences. The yeast is used for the production of human and mammalian high mannose glycoproteins with high yield and purity. The method is also useful for producing hybrid or complex sugar chains containing mammalian type chains. This sequence represents a mouse anti-human G-CSF antibody heavy chain used in the invention.
                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 416
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6-mannosyl transferase; alpha-1; 2-mannosidase; orotidin-5'-phosphate decarboxylase; URA3; orotidin-5'-phosphate decarboxylase; URA3; phosphoribosyl-amino-imidazole uccinocarboxamide synthase; ADE1; imidazole-glycerol-phosphate dehydratase; HIS3; 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PEP4; YPS1; KTR1; MNN9; AOX; GAPDH; mannosyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing methylotroph yeast disrupting the OCH1 gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-854401/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2003; 2003WO-JP005464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003091431-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methylotroph yeast; mammalian sugar chain; OCH16-mannosyl transferase; alpha-1; 2-mannosidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM47075 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KIRI ) KIRIN BEER KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-2002; 2002JP-00127677.
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   80
                                                                                                                                                                                                                                              416;
                                                      61
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                                                                                                                                                                                μ
                                                                                                                                                                                                                                                                                 Similarity
SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL----GTYYF---DSWGQGT:
                                                                                                                                                                                EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                                                                                                                                                                                                                                                                                                                        475 AA;
                                                                                                                          EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYIYY
                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                          71.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that expresses mammalian sugar chains by inserting an alpha-1,2-mannosidase gene.
                                                                                                                                                                                                                                                                          Score 2209.5;
Pred. No. 3.76
                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                          5; DB 7;
3.7e-105;
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                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                    Length 475;
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ARASTOUT 14
ARASTONE 14
ARASTONE 15-MA
DT 25-MA
DT 25-MA
DT 25-MA
DT 24-JU
XX Chime
KW Chime
KW Crans
XX Synth
XX W0932
PN W0932
XX W15-JU
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                   The sequences (AAQ54651-52) show the light and heavy chain cDNAs of murine T84.12. The T94.12 antibody is directed against the tumour marker carcinoma embryonic antigen, and is useful for tumour imaging and immunotherapy. The amino acid sequence given in the specification has been incorrectly identified as a nucleic acid sequence, therefore unacceptable characters have been represented as an 'N'. The amino acid sequence given below has been derived from the cDNA, by the indexer. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                  New chimeric T 84.12 antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also DNA encoding it and transformed myeloma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region; transform; myeloma cell; light chain; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shively JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YANG/)
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24-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-007204/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR47453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR47453 standard; protein; 477 AA.
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RESULT 15
ADM72029
ID ADM72
XX ADM72
XX ADM72
XX Chime
XX GPC3;
KW GPC3;
KW CYtos
OS Homo
OS Chime
PN WO200
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Mus sp.
Antibody against the N terminus of glypican 3 (GPC3) disruption and is useful as an anticancer agent.
                                                          WPI; 2004-269573/25.
N-PSDB; ADM72028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer; cytostatic; M19B11.
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                                                                                                                                                                                                                                             04-SEP-2003; 2003WO-JP011318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric mouse-human antibody M19B11 heavy chain.
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                                                                                                                         Aburatani
                                                                                                                                                             (CHUS ) CHUGAI SEIYAKU KK.
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Pred. No. 6.3e-105;
8; Mismatches 18;
                                                                                                                     Nakano
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                                                                                                                                                                                                                                                                                                                                                              Query Match 71.8%;
Best Local Similarity 92.3%;
Matches 418; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antibody against the N terminus of glypican 3 (GPC3). The antiboduy can be used for causing cell disruption and can be uses as an anti-cancer agent. The present sequence represents a chimeric mouse-human antibody M19B11 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 14; 122pp; Japanese
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439
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SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                                                                                                             QSSGLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
                                                                                                                                                                                                                                                                        PDTMKDRFTISRDNAKNTLYLOMNSLRSEDTAFYHCTRHN-GGYENYGWFAYWGQGTLVT
                                            RDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                       RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                        QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                    QYNSTYRVVSYLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                               QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
                                                                                                                                                                                                                                                                                                                                                              ; Score 2203.5; pred. No. 7.5e. 9; Mismatches
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7.5e-105;
les 21;
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Search completed: December 23, 2004, 18:57:43
Job time: 157.692 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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  Score
                                                                                                                                                                                                                                                                                                                                                                                                                        id. No. is the number of results predicted by chance to have a
are greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match
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   IBBUEd_Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-027-449-71
US-09-026-985-71
US-09-121-552A-71
US-09-234-340A-71
US-08-466-153B-8
US-08-466-153B-8
US-08-887-352B-14
US-08-887-352B-16
US-08-887-352B-16
US-09-109-207C-16
US-09-109-207C-16
US-09-109-207C-16
US-09-109-207C-16
US-09-171-14
US-09-296-005-14
US-09-16-028-16
US-09-171-16-028-16
US-09-171-16-028-16
US-09-171-13-996-14
US-09-171-13-996-14
US-09-171-13-996-14
US-09-18-028-16
US-09-18-028-18
US-09-109-207C-18
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Sequence 7, Appli
Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 8, Appli
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Sequence 8, Appli
Sequence 14, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 18, Appl
Sequence 18, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 18, Appl
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28 2118 69.0 451 4 US-09-282-846-2 Sequence 2, Appli 29 2118 69.0 451 4 US-09-680-145-2 Sequence 2, Appli 30 2118 69.0 451 4 US-09-920-171-18 Sequence 18, Appl 31 2118 69.0 451 4 US-09-916-028-18 Sequence 18, Appl 32 2118 69.0 451 4 US-09-483-588-2 Sequence 2, Appli

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RESULT 2
US-09-027-449-71
COMPUTER: 13.5 inch. 1.44 Mb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION NUMBER: 60/074,330
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION NUMBER: 60/038,664
APPLICATION NUMBER: 60/038,664
APPLICATION NUMBER: 40/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD 8
REGISTRATION NUMBER: 91085R3-2
TELEPHONE: 650/225-5330
TELEPHONE: 650/225-5330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 71,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gonzal
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
STREET: 1 DNA WAY
CITY: South San Franci
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                        South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genentech, Inc.
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US-09-026-985-71
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                                                                                                                                                                                                                                                                         APPLICANT: Gonzalez, Tania R.
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fr.
ITILE OF INVENTION: Humanized Ar
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 71, Application US/09026985 Patent No. 6133426
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb fl.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/99/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT IN
                                                                                                                                                                                          ADDRESSEE: Genented STREET: 1 DNA Way CITY: South San Fra STATE: California COUNTRY: USA
                                                                                                                                                                             ZIP: 94080
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San Francisco
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INFORMATION:

US/09/026,985

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Fragment-Polymer Conjugates and d Anti-IL-8 Monoclonal Antibodies

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                     RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                      DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                     SSGLYSLSSVVTVPSSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                      SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
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                                                                                                                                                                                       YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                        GGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                   EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                               YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                   GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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88.7%;
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Pred. No. 2.66
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RESULT 4
US-09-121-952A-71
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TELEPHONE: 650/225-5530
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                             Sequence 71, Application US/09121952A Patent No. 6458355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.0%;
Best Local Similarity 88.7%;
Matches 401; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Genent
APPLICANT: Koumen:
APPLICANT: Leong,
                                                                                                                                          APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
COMPUTER: IBM PC compatible
                                                                STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                  ADDRESSEE:
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Koumenis, Iphigenia
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                                                                                                                                Genentech, Inc.
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RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A.
; Patent No. 6468532
; PAPLICANT: Genentech, Inc., Heei, VE
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Preeta, Leonard G.
; APPLICANT: Shahrokh, Zahra
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SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acide
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 401; Conservative
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/121,95
FILING DATE: 24-Uul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/074330
FILING DATE: 22-TAN-1998
PRIOR APPLICATION UMBER: 60/075467
FILING DATE: 20-FEB-1998
PRIOR APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R,
TELEPAN: 650/225-5530
TELEPAN: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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                                                                                       358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Pred. No. 2.6e-159;
452
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RMATION.
Genentech, Inc.,
Koumenis, Iphigenia
Koumenis, Iphigenia
Leong, Steven R.
Leong, Steven G.
Presta, Leonard G.

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US-09-234-340A-71
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/
FILING DATE: 24-U1-1998
APPLICATION NUMBER: 60/074
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
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TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
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STREET: 1
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California
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 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                      DELTKNOVSLTCLVKGFYFSDIAVEWESNGOPENNYKTTFPVLDSDGSFFLYSKLTVDKS
                                                                                                                                            GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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                                                                                                                                                                                                                   SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
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                                                                       YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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Pred. No. 2.6e-159;
9; Mismatches 29;
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US-08-466-151-8
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Best Local Similarity
Matches 403; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb flc
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/466163
APPLICATION NUMBER: 08/466163
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 26-JOAN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JOAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
PRIOR APPLICATION NUMBER: 07/879495
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APPLICANT: Jardieu,
APPLICANT: Presta, I
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/744
PILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
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SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
                                                                          YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV
                                                                                                                             EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
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88.8%; Pred. No. 2.6e-157;
tive 21; Mismatches 24;
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PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 8
LENGTH: 453
TYPE: PRT
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing th
FILE REPERENCE: PO718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
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Best Local Similarity
Matches 403; Conserva
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SEQ ID NO 8
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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88.8%; Pred. No. 2.6e-157;
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; Sequence 8, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Dis
; FILE REFERENCE: P0718P2C2US
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
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PRIOR FILING DATE: 1994-01-26
PRIOR FPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1992-05-07
PRIOR PPLICATION NUMBER: US 07/744,768
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US-09-802-077-8
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 69.2%; Score 2124; DB 4;
Similarity 88.8%; Pred. No. 2.6e-157;
03; Conservative 21; Mismatches 24;
                                                                                                                                                                                                 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                                                                             LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE
                                                                   SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
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RESULT 10
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; PATENT NO. 1994511
; PATENTION: IMPORMATION: Improved Anti-IgE Antibodies and Method of ITILE OF INVENTION: Improved Anti-IgE Antibodies and Method of UNIVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
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Best Local Simi
Matches 401;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb flo

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,352E

FILING DATE: 03-Jul-1997

CLASSIFICATION: 530

ATTORNEY/ACENT INFORMATION:

NAME: SYODODA, Craig G.

REGERENCE/DOCKET NUMBER: 91123

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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STREET: 1 DNA Way
CITY: South San Fra
STATE: California
COUNTRY: USA
ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
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                  DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                            GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                     YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                       YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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88.7%; Pred. No. 3.7e-157;
tive 21; Mismatches 26;
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US-08-887-352B-16
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Best Local Similarity
Matches 401; Conserv
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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CURRENT APPLICATION DATA:
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TYPE: A
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Amino Acid
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                YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
                                                                                 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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                                                                GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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1 DNA Way
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                                                                                                                                                                                                                                                                                                                                                                                                                           69.1%; Score 2122; DB 2; 88.7%; Pred. No. 3.7e-157;
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Improved Anti-IgE Antibodies and Method of
Improving Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P1123
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 451;
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                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                    Matches 401;
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Patent No. 60374
                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650/225-14
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/466:
APPLICATION NUMBER: 08/405:
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405:
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/185:
PILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda Crain
                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                            NAME: SVODOđA, CRAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PO:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: (
FILING DATE: 07-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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                 60 YSDSVKGRFTISRDNAKNTLYLØMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
                                                                                                 1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
                                                                                                                                                                        Similarity
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YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV
                                                                     EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIROAPGKGLEWVASITYDGS-TN
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Sequence 14, Application US/09109207C

Patent No. 6172213

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
IIILE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: p1123R1

CURRENT FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 14

LENGTH: 451

TYPE: PAT

ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-451

COTHER INFORMATION: Heavy chain sequence derived from MAE11

US-09-109-207C-14
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Sequence 16, Application US/09109207C

Patent No. 6172213

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula
ITILE OF INVENTION: Improved Anti-IgE Antibodies and
FILE REFERENCE: P1123R1

CURRENT APPLICATION NUMBER: US/09/109,207C

CURRENT FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554

PRIOR APPLICATION NUMBER: US 60/051,554

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 16

LENGTH: 451

TYPE: PRI
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: Artificial
; LCCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16
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US-09-109-207C-16
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; Pred. No. 3.7e-157;
21; Mismatches 26;
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; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14
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US-09-296-005-14
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Patent No. 6290957

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r

CURRENT APPLICATION NUMBER: US/09/296,005

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 08/887,352

EARLIER FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 14

LENGTH: 451

TYPE: PRT

ORGANISM: Artificial

FEATURE:

PRT

ORGANISM: Artificial

FEATURE:

NAME/FEV. Artificial
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       2744.5
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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Sequence 41, Appl
Sequence 32, Appli
Sequence 6, Appli
Sequence 37, Appl
Sequence 37, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 62, Appli
Sequence 64, Appli
Sequence 6, Appli
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<b>4</b> 5	44	43	2	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/37,113
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/371,966
PRIOR APPLICATION NUMBER: 60/371,966
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 579
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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publication No. US20030166163A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Immunocytokines With Modulated
FILE REFERENCE: LEX-020
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 515; Conserv
                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: dI-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant-10-310-719-32
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                                        ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                        SDSVKGRFTISRDNAKNTLYLQMRSLRSBDSAMYFCTR-VKLGTYYFDSWGQGTTLTVSS
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30; Mismatches 33; I
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Best Local Similarity
Matches 517; Conserv
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FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/433,945
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 575
                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2
US-10-737-208A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gillies, Stephen D.
APPLICANT: Lo, Kin-Ming
TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES
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SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                        STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
                                                                                                                           STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
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Pred. No. 9.5e-
24; Mismatches
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477 479 417

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Sequence 37, Application US/10310719

Publication No. US20030166163A1

GENERAL INFORMATION:
APPLICANT: Gillles, Stephen
ITITLE OF INVENTION: Immunocytokines With Modulated Sel
FILE REFERENCE: LEX-020

CURRENT APPLICATION NUMBER: US/10/310,719

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 60/37,113

PRIOR APPLICATION NUMBER: 60/37,113

PRIOR FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 60/371,966

PRIOR FILING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.1

SEQ ID NO 37

LENGTH: 580

TYPE: PRT

ORGANISM. Artificial Screens
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US-10-310-719-37
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Best Local S
Matches 494
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nes 494; Conservative
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                PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQAQ
                                   PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
                                                                                                                                                            ASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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84.7%; Pred. No. 7.1e-157;
7ative 31; Mismatches 54;
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Publication No. US20030166163A1

GENERAL INPORMATION:

APPLICANT: Gillies, Stephen

TITLE OF INVENTION: Immunocytokines With Modulated Sel

FILE REFERENCE: LEX-020

CURRENT APPLICATION NUMBER: US/10/310,719

CURRENT ILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 60/337,113

PRIOR APPLICATION NUMBER: 60/337,113

PRIOR APPLICATION NUMBER: 60/371,966

PRIOR FILING DATE: 2001-12-04

PRIOR FILING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 37

NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: dI-NHS76 (gamma2h) (FN>AQ)-ala-IL2(D20T) heavy chain fused to US-10-310-719-35
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPETH: 580
TYPE PRT
ORGANISM: Artificial Sequence
PEATURE:
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                                                                                                                                                                                                                                    120 -ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
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NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
                                                                                                                                                              SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
                                                                                                                                                                                                                  GASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                                                            EVTLVESGGDFVKPGGSLKVSCAASGFAFSH-YAMSWVRQTPAKRLEWVAYISSGGSGTY
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                                                                                   GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
                                                                                                                                                                                                                                                                                      YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGKWSK--FDYWGOGTLVTVSS
                                                                                                                                                                                                                                                                                                                    YSDSVKGRFTISRDNAKNTLYLOMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                                                                                                           QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGS-TY
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                                                                      GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQA
                                                                                                                                           SGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVEPKSCDKTHTCPPCPAPP-VA
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                                                                                                                                                                                                                                                                                                                                                                                                                              83.4%; Score 2560; DB 14;
84.1%; Pred. No. 7.8e-155;
Live 31; Mismatches 56;
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Gaps

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CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR PELICATION NUMBER: 60/275,289
PRIOR RELING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR PILING DATE: 2001-06-21
PRIOR PILING DATE: 2001-06-21
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
VUMBER OF SEQ ID NOS: 33
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 663
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US-10-412-406-32
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Best Local Similarity
Matches 418; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LYNE, Paul
APPLICANT: SALDHANA, Jose W.
TITLE OF INVENTION: HUWANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINALOGEN
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APPLICANT: GARBER, EL
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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPESRDE
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                                                            PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVBVHNAKTKPREEQYN
                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                     GLYSLSSVVTVPSSSLGTQTY I CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                           PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                                                                                                               72.2%;
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TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTI-LILE REPERENCE: BINALOCN
CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2001-03-13
PRIOR PELICATION NUMBER: 60/275,289
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 33
SOPTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 4852
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US-10-412-406-33
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Best Local Similarity 93.1%;
Matches 418; Conservative
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APPLICANT: GARBER, Ellen
APPLICANT: LYNE, Paul
APPLICANT: SALDHANA, Jose
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                                                                   360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
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QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
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Pred. No. 5.4e-132;
9; Mismatches 21;
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RESULT 9
US-10-679-620-62
; Sequence 62, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Large Scale Biology
APPLICANT: Reinl, Stephen J.
APPLICANT: Rewards, Patricia C.
APPLICANT: Rewards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
PILE REFERENCE: 34150-004A
CURRENT FILING DATE: 2003-10-03
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTMARE: Patentin version 3.2
SEQ ID NO 64
LENGTH: 713
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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US-10-679-620-64
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 64, Application US/10679620 Publication No. US20040110930A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                              LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 412
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                                                                                                                                                                        TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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ilarity 91.7%;
Conservative 10
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; Pred. No. 8.2e-133;
10; Mismatches 20;
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                                             APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: ANTHODIES TO VLA-1
FILE REFERENCE: A101 PCT
CURRENT APPLICATION NUMBER: US/10/474,832
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/283,794
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/303,689
PRIOR APPLICATION NUMBER: 60/303,689
PRIOR PILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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US-10-474-832-4
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                                                                                                                                                                                                                                                                   Sequence 4, Application Publication No. US200400
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SEQ ID NO 62
LENGTH: 715
TYPE: PRT
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Best Local
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LENGTH: 447
TYPE: PRT
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING FILE REFERENCE: 34150-004A CURRENT APPLICATION NUMBER: US/10/679,620 CURRENT FILING DATE: 2003-10-03 PRIOR APPLICATION NUMBER: 60/415,940 PRIOR FILING DATE: 2002-10-03 NUMBER OF SEQ ID NOS: 122 CONTRACTOR SECOND N
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                                                                            TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 715
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; Pred. No. 8.3e-133;
10; Mismatches 20;
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APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cytotoxic CD44 Antibody Imperior CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US/80/307,451
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 444
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                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Humanised; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: US-10-150-475A-6
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US-10-150-475A-6
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Best Local Similarity
                                                               Matches
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Best Local (
                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVST1SSGGSYTYY
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                                                                          71.7%;
                                                          Score 2200.5;
Pred. No. 4.6e
11; Mismatches
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Pred. No. 4e-132;
9; Mismatches 2
                                                          00.5; DB 14;
. 4.6e-132;
tches 18; I
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APPLICANT: Adolf, Gunther
APPLICANT: Baumann, Michael
APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and methods for
TITLE OF INVENTION: Cytotoxic CD44 Antibody Imm
FILE REFERENCE: 1/1414
CURRENT APPLICATION NUMBER: US/10/704,522
CURRENT APPLICATION NUMBER: US 60/429,516
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US 60/429,516
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIAN OF 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
CURANTSM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10704522 Publication No. US20040120949A1 GENERAL INFORMATION:
                                                                                                                                                                                                                Matches 415;
                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy
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                              STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
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 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
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Pred. No. 4.6e-132;
1; Mismatches 18; I
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FILE REFERENCE: 1/1383
CURRENT APPLICATION NUMBER: US/10/645,215
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: EP 02 018 686.2
PRIOR FILING DATE: August 21, 2002
PRIOR APPLICATION NUMBER: US 60/405,956
PRIOR FILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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US-10-645-215-6
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US-10-645-215-6
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Best Local S
Matches 415
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Publication No. US20040126379A1
GENERAL INFORMATION:
APPLICANT: Adolf, Guenther
APPLICANT: Heider, Karl-Heinz
APPLICANT: Heider, Karl-Heinz
APPLICANT: Holder, Karl-Heinz
APPLICANT: Heider, Heinz
APPLICANT: Hein
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ORGANISM: Artificial Sequence
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Similarity 92.4%; Pred. No. 4.6e-132;
15; Conservative 11; Mismatches 18; Indels 5;
                                                                                                                                                                                                      LYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
                                                                                                                                                                                                                                                                               STKGPSVPPLAPSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSSG 175
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                                                                                       SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
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Publication No. US20040219633A1

GENERAL INFORMATION:

APPLICANT: Bolhnis, Reinier LH
APPLICANT: Woehl, Thorsten

APPLICANT: Boettger, Volker

TITLE OF INVENTION: Method of Producing Recombinant Antibodies

FILE REFERENCE: 2923-552

CURRENT APPLICATION NUMBER: US/10/635,908

CURRENT APPLICATION NUMBER: PCT/EP02/01283

PRIOR APPLICATION NUMBER: ECT/327,008

PRIOR FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 60/327,008

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/266,853

PRIOR FILING DATE: 2001-02-07

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.2

LENGTH: 449
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US-10-635-908-16
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US-10-635-908-16
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26. TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
356 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415
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Similarity 92.2%;
  QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                       TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                                                                                      TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
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                                                       TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
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; Pred. No. 7.8e-132;
14; Mismatches 21;
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RESULT 15
US-10-635-908-18
US-10-635-908-18
; Sequence 18, Application US/10635908
; Publication No. US20040219633A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bolhuis, Reinier LH
; APPLICANT: Bolhuis, Reinier LH
; APPLICANT: Woehl, Thorsten
APPLICANT: Woehl, Thorsten
; TITLE OF INVENTION: Method of Producing Recombinant Antibodies
; FILE REFERENCE: 2923-552
; CURRENT APPLICATION NUMBER: US/10/635,908
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: PCT/EP02/01283
; PRIOR APPLICATION NUMBER: PCT/EP02/01283
; PRIOR APPLICATION NUMBER: 60/327,008
; PRIOR APPLICATION NUMBER: 60/366,853
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEC IN NOG. 23-07
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SOFTWARE: PATENTIN version 3.2
SEQ ID NO 18
LENGTH: 449
TYPE: PAT
ORGANISM: Artificial
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.5%; Score 2197; DB 17; Best Local Similarity 92.2%; Pred. No. 7.8e-132; Matches 414; Conservative 14; Mismatches 21;
                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                              121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPBPVTVSWNSGALTSGVHTFPAVLQSSG 180
121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPBPVTVSWNSGALTSGVHTFPAVLQSSG 180
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                                                                                                                                                                                                                                                          TYRVVSVLTVLHQDWLMGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            pir 79:*
1: pir1:*
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Gapop 10.0 , Gapext 0.5
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3071
1 EVTLVESGGDFVKPGGSLKV.....IVEFLNRWITFCQSIISTLT 582
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## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	0	7	6	ഗ	4.	ω	N	_	Result No.
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398	393	329	324	333	289	326	308	329	328	323	328	234	328	255	328	475	474	472	446	374	469	470	444	327	326	377	377	330	Length
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G3MSM	GIMSM	G3MSC	GIMS	PS0018	G3HUWI	PS0017	C30554	G2GP	I47161	GHRB	I47158	PT0207	I47160	S31866	I47159	S01321	G2MS11	831459	S40295	869339	S37483	S22080	PC4436	G4HU	G2HU	A60764	A23511	GHHU	ID
gamma-3 chain	Ļ	gamma-3 chain	1 chain	_	gamma-3	gamma-1 chain	heavy chain C	gamma-2 chain	gamma 3 chain	gamma chain C	gamma 1 chain	gamma cha	gamma 2b	gamma-1 c	_	gamma-2b		gamma-1	gamma			-	noclonal antibo	gamma - 4	gamma-2 chain	gamma-3 chain	gamma-3 chain	mma-1 chain	Description

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330 1 GZMSA 335 1 GZMSAB 19 399 1 GZMSAB 19 399 1 GZMSAM 19 548 2 S308847 19 548 2 S38864 19 322 2 PS0019 19 327 2 S06611 19 405 1 GZMSBM 19 277 2 147162 19 549 2 S04845 19 549 2 S04845 19 549 2 S69340 19 572 2 B46529 19 572 2 B46529 19 241 2 S69131 19 241 2 369131 19 254 2 B46529 19	744.5	760	770	801.5	802.5	817.5	845.5	1066	1082	1092.5	1112	1118	1118.5	1121	1123.5	1126
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	Ig heavy cl	Ig gamma-1	Ig heavy cha	Ig heavy chai	Ig Y heavy ch	Ig heavy chai	Ig heavy chai:	Ig gamma 4 cha	Ig gamma-2b ch	Ig gamma-2 cha	Ig gamma-2a ch	Ig epsilon cha	Ig gamma-2c ch	Ig gamma-2a ch	_	Ig gamma-2a ch

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m. 357, 1571-1604, 1976	Hope-Seyler's Z. Physiol. Chem. 357, 1571-1604,
A;Accession: A90564 A;Accession: type: protein A;Molecule type: protein A;Residues: 136-154, Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240 A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met	A;Accession: A90564 A;Molecule type: protein A;Residues: 136-154, Q', 156-16 A;Residues: this sequence has the
e of a human gammaG-immunoglobulin. VIII. Amino acid sequ ID:71064025; PMID:5530842	A;Title: The covalent structure of a human gammaG-immun A;Reference number: A90564; MUID:71064025; PMID:5530842 A;Contents: Eu
A;Note: this sequence has the Glm(3) marker, 97-Arg R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M. Biochemistry 9, 3171-3181, 1970	A;Note: this sequence has the R;Rutishauser, U; Cunningham, Biochemistry 9, 3171-3181, 197
UN>	A;ACCEBBION: B9U563 A;Molecule type: protein A;Residues: 1-96,'R',98-135 <cun></cun>
ture of a human gammaG-immunoglobulin. VII. Amino acid seque MUID:71064024; PMID:5489771 Eu	A; Title: The covalent structure of a human A; Reference number: A90563; MUID:71064024; A; Contents: myeloma protein Eu
r, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, 0	A;Cross-rerences: EMBL:21/370 R;Cunningham, B.A.; Rutishauser, Biochemistry 9, 3161-3170, 1970
**>	A; Molecule type: DNA A; Residues: 88-113; 235-330 < TAK>
munoglobulin gamma genes: implications for evolution of a TD:83001943; PMID:6811139	A;Title: Structure of human immunoglobulin gamma genes: A;Reference number: S33887; MUID:83001943; PMID:6811139 A;Accession: S33887
ta, M.; Nikaido, T.; Nakai, S.; Honjo, T.	A;cross-reterences: EMBL:Z17370 R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, Cell 29, 671-679, 1982
	A; Molecule type: DNA A; Residues: 2-330 <har></har>
rary, October 1992	submitted to the EMBL Data Library, October 1992 A;Reference number: S33904 A;Accession: S36861
GIm(17) allotypic marker, 97-Lys, and the Gim(1) markers, er translation	A.Note: this sequence has the Glm(17) allotypic A.Note: Lys-330 is removed after translation R.Harris, L.J.
1857. EMRT. 217370	A; Molecule type: DNA A; Residues: 1-330 <ell> A: Cross-references: INITEROT: D01857. EMRI: 217370</ell>
ice of a human immunoglobulin C-gammal gene. IID:82274238; PMID:6287432	A; Title: The nucleotide sequen A; Reference number: A93433; MU A-Accession: A93433
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J. Hood, L.E. Nucleic Acids Res. 10. 4071-4079, 1982	C;Accession: A93433; S36861; S R;Ellison, J.W.; Berson, BJ, Nucleic Acids Res. 10. 4071-40
man xevision 18-Aug-1982 #text change 09-Jul-2004	Ig gamma-1 chain C region - human C;Species: Homo sapiens (man) C:Date: 31-Jan-1981 #secuence rev
/	RESULT 1
ALIGNMENTS	
2 A49444 Ig gamma-1 heavy c 2 B31790 Ig heavy chain V r	44 760 24.7 220 45 744.5 24.2 254

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A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents wyeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, (V, 36-96, 'K', 98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A;Reference number: A91723; MUID:83389131; PMID:884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A9173
A;Molecule type: protein
A;Residues: 1-96, RY, 98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Residues: 1-96, RY, 98-197,'D',199-238,'E',240,'
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F;137-206/Domain: immunoglobulin homology <IM2>
F;137-206/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental F;103/Disulfide bonds: interchain (to light chain) #status experimental F;103/Disulfide bonds: interchain (to heavy chain) #status experimental F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
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A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; CMIM:147100
A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;20-85/Domain: immunoglobulin homology <IM1>
F;20-85/Domain: immunoglobulin homology <IM1>
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ilarity 100.0%;
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Pred. No. 2.6e-92;
0; Mismatches 0;
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Ig gamma-3 chain C region (allotype G3m(b)) - human C;Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change : C;Accession: A25511 R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 1779-1789, 1986 Nucleic Acids Res. 14, 1779-1789, 1986 A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain (A;Reference number: A23511; MUID:86148507; PMID:3081877 A;Accession: A23511 A;Molecule type: DNA A;Residues: 1-377 <HUC> A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA277 C;Genetics: C;Genet
                                                                                                                                                                                                                                                            Ig gamma-3 chain C region, form LAT C;Species: Homo sapiens (man) C;Species: 14-May-1993 #sequence_revis C;Accession: A60764 R;Huck, S; Lefranc, G; Lefranc, l Immunogenetics 30, 250-257, 1989
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Crose-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C rec
C;Keywords: immunoglobulin
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A;Cross-references: GDB:119339; OMIM:147120
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
C;Keywords: immunoglobulin homology <IMM>
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A23511
                                                                                                                                                                            Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele
A;Reference number: A60764; MUID:90007613; PM
A;Accession: A60764
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10; Mismatches
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A;Molecule type: protein
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193,'D', 195-325 <A
A;Residues: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NI
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Eudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain:
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobul
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
                                               A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B'
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
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A;Residues: 1-326 <ELL>
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;Title: A note on the amino acid sequence ;Reference number: A93132; MUID:80114419;
                                     ;Hofmann, T.; Parr, D.M.
ol. Immunol. 16, 923-925, 1979
                                                                                                                                       ;Contents: myeloma protein;Accession: A90752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
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Pred. No. 1.9e-84;
0; Mismatches 11
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  of residues 381-391
PMID:118920
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                                                                                               ,177-193,'D',195-196,'Q'
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                  of human
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                  immunoglobulin
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R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of A;Reference number: A90253; MUID:72033500; PMID:44
A;Contents: annotation; myeloma protein Sa, disult R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A93132
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;239-306/Domain: immunoglobulin homology <IM3>
F;27-83,140-200,246-304/Disulfide bonds: #status experimental F;27-83,140-200,246-304/Disulfide bonds: #status experimental F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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les 301; Conservative
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                        QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                           LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
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                                                                                  MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                       STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE
                                                                                                                                                                                             STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                       PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN
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Pred. No. 3.7e-83;
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PMID:4940472
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PMID:5782707
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Ig gamma-4 chain C region - human c;Species: Homo sapiens (man) C;Date: 02-Apr-1982 #Bequence revision C;Accession: A90933; A90249; A02150 R;Ellison, J.; Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981 DNA 1, 11-18, 1981

02-Apr-1982

#text\_change

09-Jul-2004

human

immunoglobulin

C-gamma4

RESULT G4HU

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A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14932.33-14932.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin (C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;91-10/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;140-307/Domain: immunoglobulin homology <IM3>
F;147/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;105,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_cha
C;Accession: PC4436
R;Akashi, S; Kato, K; Torizawa, T.; Dohmae, N.; Yamaguchi,
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal ant
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
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A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Residues: 1-327 <ELL>
A;Cross-references: UNIRROT:P01861
A;Cross-references: UNIRROT:P01861
A;Note: the sequence was determined from the (R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M., Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Para;Reference number: A90249; MUID:70207560; PM.
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
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Matches 300
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Species: Mus musculus (house mouse)
State: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                             QEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG
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Pred. No. 2.1e
12; Mismatches
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2.1e-82;
hes 15;
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A; Accession: $06610
A; Accession: $06610
A; Molecule type: DNA
A; Residues: 142-470 <SYM>
A; Cross-references: EMBL:X16701
A; Cross-references: EMBL:X16701
A;Note: the sequence was determined from to;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
A;Superfamily: immunoglobulin C region; im C;Kuywords: glycoprotein; heterotetramer; F;161-225/Domain: immunoglobulin homology
                                                                                                                                                                                                    A;Status: preliminary
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-470 <SANA
A,Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1;
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1;
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1;
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1;
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1;
A;Reference number: S06610; MUID:90097956; PMID:2513487
                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovin N;Alternate names: Ig gamma-1 chain C region (clone C;Species: Bos primigenius taurus (cattle) C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 C;Accession: S22080; S06610; A31303 R;Sanders, P.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: This catalytic antibody has peroxidase oxidase activity. C;Superfamily: immunoglobulin C region; immunoglobulin homology F;251-320/Domain: immunoglobulin homology <IMM> F;251-320/bsulfide bonds: interchain (to 98) #status predicted F;99/Disulfide bonds: interchain (to 109) #status predicted
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Pred. No. 1.4e
74; Mismatches
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                                      immunoglobulin homology
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                   immunoglobulin;
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l.4e-77:
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submitted to the EMBL Data Library, February 1993
A;Reference number: $37483
A;Recession: $37483
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-469 < DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; Cysuperfamily: immunoglobulin
C;Superfamily: immunoglobulin
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
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PGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKPREE
                                      ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
                                                                                                                                                             DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYGEVGDGAIADAWGQGLLVT
                 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD
                                                                                                              SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT-YYFDSWGQGTTLTVSS
                                                                                                                                                                                                 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
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                                                                                         NENFKGKATLTVDTSSSTAYMOLSŠLTŠEDTAVY FCARAMGATATLLDYWGQGTTLTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OVOLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWVGGITSGGT-TYY
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                                                                                                                                                                                                                                    Score 1430.5; DB:
Pred. No. 3.2e-73;
71; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1466; DB 2;
Pred. No. 3.3e-75;
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                                                                                                                                                                                                                                       110;
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                                                                                                                                                                                                                                                                           469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Khamlichi, A.A.
submitted to the EMBL Data
submitted to number: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
C;Accession: S69339; S72664
R;Khamlichi, A.A., Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
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A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
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A; Residues: 1-374 < KHA>
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                                                                                           LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWXVDGVEVHNAKTKPRE
                                                                                                                                                                   LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE
                                                                                                                                                                                                                                                        TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
                                                                                                                                                                                                                                                                                           RYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQGTLV
                                                                                                                                                                                                                                                                                                                         YYSDSVKGRFTISRDNAKNTLYLOMRSLRSEDSAMYFCTRVKLG----TYYFDSWGQGTTL
                                                                                                                                                                                                                                                                                                                                                                 QITLKESGPTLVKPTQTLTLTCTPSGFSLSKSGVGVGWIRQPPGQALEWLALI-FWDDDK 78
                                                                                                                                                                                                                                                                                                                                                                                                     EVTLVESGGDFVKPGGSLKVSCAASGFAFSH--YAMSWVRQTPAKRLEWVAYISSGGSGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         46.3%; Score 1423; DB 2; llarity 61.9%; Pred. No. 6.4e-73; Conservative 23; Mismatches 46;
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted F;132/Disulfide bonds: interchain (to light chain) #status predicted F;224,227,229/Disulfide bonds: interchain #status predicted F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental
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F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
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C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology.
C;Superfamily: immunoglobulin C region; immunoglobulin; pyrog-
C;Keywords: disulfide bond; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein;
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A; Accession: S40295
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A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 a
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                                                                                                                                                                                                                                                                                                        LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLG
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                                                                                                   NSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEE
                                                                                                                                                                                                    GPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDY
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                                                                    Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H. submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inacti
                                                                                                                                                                                                                                                      RESULT 12
G2MS11
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S31459
                       A; Reference number: S25057
A; Accession: S25057
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preliminary
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Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis am
C;Date: 13-Jan-1995 #sequence_revision 13
C;Accession: S31459
R;Patri, S; Nau, F.
submitted to the EMBL Data Library, Decem
A;Reference number: S31459
A;Accession: S31459
A;Accession: S31459
A;Accession: S31459
A;Residues: 1-472 < PAT>
A;Residues: 1-472 < PAT>
A;Residues: 1-472 < PAT>
C;Superfamily: immunoglobulin C region; i
C;Keywords: immunoglobulin homology
F;277-346/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 269; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                               QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                   TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
YSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK
                     YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                               YVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADGSYFL
                                                                                                       YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFL
                                                                                                                                                                 TKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQV
                                                                                                                                                                                    TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                             CPPPELPGGPSVPIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTAR
                                                                                                                                                                                                                                                                                                                           TFPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHC-R
                                                                                                                                                                                                                                                                                                                                                                                                           PGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TYYSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY-----FDSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWL----
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Pred. No. 3.5e-
66; Mismatches
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13-Jan-1995
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3.5e-72;
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inactivating H.J.;

neotop specific

09-Jul-2004

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A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Contents: DNA
A;Contents: A3598; MUID:94216359; PMID:7512967
A;Contents: DNA
A;Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Contents: description
A;Contents: CB:J00461
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM'>
A;Contents: CB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hub.
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TUI>A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunog:
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
A;Molecule type: DNA
A;Residues: 138-173,'P',174-189,'FP',193-376,'T',378-474 <TU2>
A;Holecule type: DNA
A;Residues: 138-173,'P',174-189,'FP',193-376,'T',378-474 <TU2>
A;Title: Mouse immunodiobulin allotypes: post-duplication divergence of gamma2a and gar
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A;Residues: 1-474 <FIS>
A;Residues: 1-474 <FIS>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.1;
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
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   80
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NEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCAR----DYDYDWFAYWGQGTLVTV
                                                                                                                                                                                                           EVTIVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY
                                                                 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY---YFDSWGQGTTLTV
                                                                                                                                  EVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDGTKF
                                                                                                                                                                                                                                                                                                         44.48;
                                                                                                                                                                                                                                                                                                             Score 1365; DB 1;
Pred. No. 1.6e-69;
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RESULT 13
S01321
S01321
Ig gamma-2b chain precursor - mouse
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
C;Accession: S01321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781 A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-475 < DE1>
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A; Reference number: S01320;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                            61 SDSVKGRFTISRDNAKUTLYLQMRSLRSEDSAMYFCTRVK-LGTYYFDSWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.; Feys, V.; van de Voorde,
chem. 176, 287-295, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                      APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCPPCKECHKCP
                                                                                                                                                                                                           GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP-----CP
                                                                                                                                                                                                                                                         AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLTVDKSRWQQGNVFSCSVMHEALIANHYTQKSLSLSPGK 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP-----
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                                                                     APNIEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQ
                                                                                                                                                                                                                                                                                                      ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                 NEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQVGLLPFGYWGQGTLVTASA
                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGNSYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-lymphoid cells of mouse recombinant 1320; MUID:88329081; PMID:3138116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.7%; 5c.
55.4%; Pred
5.00 75;
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Pred. No. 2.5e
75; Mismatches
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RESULT 14

147159

Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_cham
C;Accession: 147159
R;Kacskovics, I; Sun, J; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
n; Filpula, D.

submitted to the EMBL Data Library, February 1993
A; Description: Screeing method for protein-protein
A; Reference number: S31866
A; Molecule typon
                                                                                            S31866
S31866
C;Species:
C;Species:
A;Note: Hom
C;Date: 06-
C;Accession
C;Accession
C;Accession
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                                                                                                                                                                                                                                        RESULT
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;Superfamily: immunoglobulin C region; immunoglobulin
;Superfamily: immunoglobulin homology <IMM>
                                                                                                                  g gamma-1 chain C region - synthetic
;Species: synthetic
;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
;Accession: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma 2a chain constant region - pig (fragment)
¡Species: Sus scrofa domestica (domestic pig)
pate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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: |:|:::|||:| | | | |:|::| ||||
NMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 475
                                                                                                                                                                                                                                                                                                                  RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                                                                                                                                                                                                                                                                                                            LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1263; DB 2;
; Pred. No. 5.3e-64;
43; Mismatches 52;
                                                                                                                                                                                                                                                                                                328
                                                            interactions
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A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:C;Keywords: immunoglobulin
F;1-22/Region: Bscherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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Best Local Similarity
Matches 233; Conserv
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 197
                               391
                                                                137
                                                                                                331
                                                                                                                                   77
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                                                                                    PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
                 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255
                                                                                                                                                   EDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                                                                        TKVDKXVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                PAPIEKTISKAKGOPKEPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE
                                                                                                                                   EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                   41.0%;
97.5%;
                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                     Score 1260; DB 4;
Pred. No. 5.8e-64;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                   Length
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                                   449
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Search completed: December 23, 2004, 19:06:08
Job time: 33.449 secs

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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Carninci P., Prange C.,

X Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Hopkins R.F., Jordan H., Peters G.J., J., Abramgen R.D., Mullahy S.J.,

X Hopkins S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Richards S., Morley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Mhting M., Madan J.W., Green E.D., Dickson M.C.,

X Hall M., Schell B., Schnerch A., Schein J.E.,

X M., Schmutz J., Myers R.M., Butterfield Y.S.,

X M., Carnarion M.A.,

**Green E.D., Dickson M.C.,

X M., Schmutz J., Myers R.M., Butterfield Y.S.,

X M., Schmutz J., Myers R.M., Schein J.E.,

X M., Schmutz J., Myers R.M.,

**Green E.D., Dickson M., Sc
Strausberg R.;
Submitted (DEC-2001) to the E
Submitted (DEC-2001) to the E
EMBL; BC018747; AAH18747.1; -
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
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05-JUL-2004
05-JUL-2004
                                                                                                              Strausberg R. Submitted (DR
                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                              "Generation and initial analysis and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99.
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Mammalia; Eutheria;
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SMART; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS00235; IG_MHC; UNKNOWN_2.
PROSITE; PS00230; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556
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WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F AAH18747; AAH18747; 02-MAR-2004 02-MAR-2004 MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Diatchenko L., Marusina K., Framer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., SEQUENCE FROM N.A. TISSUE=Primary B-C NCBI\_TaxID=9606; 02-MAR-2004 4 (TrEMBLrel. 4 (TrEMBLrel. 4 (TrEMBLrel. 27, 27, 27, Last sequence update) Created) Craniata; Ve Catarrhini; Vertebrata; Euteleostomi; Hominidae; update)

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"Generation and intial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                           Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazos, Chordata,
Mammalia, Eutheria, Primates;
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Submitted (DEC-2001) to the
EMBL; BC018747; AAH18747.1;
SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
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                                                    NCBI_TaxID=9606;
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Last sequence that annoted
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Pred. No. 5.2e-
10; Mismatches
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                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Wagnin T.B., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RICHARDS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A., Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Willaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., RA Krzywinski M.S., Schein J.S., Schein J.S., Schein J.S., Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local S
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TISSUE=Primary
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YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                    CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                              QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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                                                                                                                                      TKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                           KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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                                                                                                             TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
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Matches 413
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K Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan H., Sonaldo M.F., Casavant T.L., Scheetz T.E.,

Brawnstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Modriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
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02-MAR-2004 (TrEMBLrel. 2
02-MAR-2004 (TrEMBLrel. 2
02-MAR-2004 (TrEMBLrel. 2
02-MAR-2004 (TrEMBLrel. 2
Hypothetical protein.
Hypothetical from (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932;
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Mammalia; Eutheria;
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                                                                                                                                   TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVVEPKSCDKTHTCPP
                                                                                                                                                                                                                                                   QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                          TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP
                                                                                                                                                                                                                    KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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Primates;
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Pred. No. 5.3e-132;
3; Mismatches 23;
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Best Local S
Matches 406
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EMBL; BX640947; CAB45972.1; -.

R InterPro; IPR003599; Ig.-1ike.

R InterPro; IPR003597; Ig_c1.

R InterPro; IPR003597; Ig_c1.

R InterPro; IPR003596; Ig_wHC.

R InterPro; IPR003596; Ig_wHC.

R InterPro; IPR003596; Ig_v.

R Ffam; PF07654; C1-set; 3.

R Pfam; SM00409; IG; 2.

R SWART; SM00409; IG; 1.

R PROSITE; PS00290; IG-MHC; UNKNOWN_2.

D SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4BBE CRC64;
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Name=DKPZp686G11190;
Homo saniaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6MZQ6 PRELIMINARY;
Q6MZQ6; PRELIMINARY;
Q5-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Human esophagus tumor;
THE GERMAN HUMAN CDNA CONSORTIUM;
Lauber J., Bahr A., Mewes H.W., Weil B.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKF
                                                                                             AVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA
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Best Local Similarity
Matches 406; Conserv
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TISSUE-Human esophagus tumor;
Lauber J., Bahr A., Mewes H.W.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae;
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ilarity 89.0%;
Conservative 1
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Pred. No. 7e-131;
8; Mismatches 25;
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       RESULT
Q6N089
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DT 05
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BAC85232
ID 85232
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Best Local S
Matches 406
Q6N089 PRELIMINARY; PRT; 472 AA. Q6N089; Q5-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation updat Hypothetical protein DKFZp686F15220.
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BAC85232;
02-MAR-2004
02-MAR-2004
02-MAR-2004
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Primata;
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Pred. No. 7
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C TISSUE-Dermoid tumor;

A Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suz A Hata H., Nakagawa S., Mizuno S., Morinaga M., Kawamura M., A Hata H., Nakagawa K., Mizuno S., Morinaga M., Nishikawa T., Sugi X. Kawakami B., Nagai K., Isogai T., Sugano S.;

RI Kawakami B., Nagai K., Isogai T., Sugano S.;

RI "NEDO human cDNA sequencing project.";

RI Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AK129776; BAC85232.1; -.

SQ SEQUENCE 472 AA; 51212 MW; 01BF215F99809164 CRC64;

SQ SEQUENCE 472 AA; 51212 MW; 01BF215F99809164 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ26265 fis, clone DMC05516, highly similar to C region.
DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                     PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                  EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                      VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
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                                                                                                                                                           EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
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                                                                              PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV
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les 23;
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RESULT 10
CAE45781
ID CAE45
AC CAE45
DT 02-MA
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Best Local S
Matches 408
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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid
Pobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ dat
EMBL; BX640627; CAE45781.1; -.

R EMBL; BX640627; CAE45781.1; -.

R InterPro; IPR003599; IG_C1.

R InterPro; IPR003597; IG_C1.

R InterPro; IPR003597; IG_G1.

R InterPro; IPR003597; IG_C1.

R InterPro; IPR003596; IG_WIGC.

R InterPro; IPR003596; IG_Y.

R Pfam; PF07654; C1-set; 3.

R Pfam; PF070647; IG; 4.

R Pfam; PF00047; IG; 2.

R SMART; SM00407; IG; 3.

R SMART; SM00407; IGC1; 3.

R SMART; SM00406; IGY; 1.

R PROSITE; PS05035; IG_LIKE; 4.

R PROSITE; PS05035; IG_LIKE; 4.

R PROSITE; PS05035; IG_MHC; UNKNOWN_2.

M Hypothetical protein.
CAE45781 PRELIMINARY;
CAE45791;
02-MAR-2004 (TrEMBLrel. 2
02-MAR-2004 (TrEMBLrel. 2
02-MAR-2004 (TrEMBLrel. 2
PAPPOCHETICAL PROTEIN DKFZ
DKFZP686P15220.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; |
NCBI_TaxID=9806;
[1]
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                                                                                                                                                                                                                                                                                 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Primates;
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el. 27, Last annotation
bkFZp686P15220.
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Pred. No. 1.8e-
16; Mismatches
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Best Local
Matches 40
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Wambutt R., Heubner D., Mewes
Pobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the E
EMBL; BX640627; CAE45781.1;
Hypotherical protein.
SEQUENCE 472 AA; 51724 MW;
                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pri
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Eukaryota, Metazoa, C
Mammalia, Eutheria, P
NCBI TaxID=9606;
[1]
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Q6GMW7;
Q5-JUL-2004
05-JUL-2004
05-JUL-2004
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.
Klausner R.D., Collins F.S., Magner L., Schaefer C.F., Bhat N.K.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Spleen;
                                                                                                                                                                                               NCBI_TaxID=9606;
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Primates;
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J. Lu X., Gibbs R.A.,

Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ketheman M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalaka U., Smallus D.E., Schmerch A., Schein J.B.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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R InterPro; IPR003597; Ig-11ke.
R InterPro; IPR003597; Ig-c1.
R InterPro; IPR003596; Ig_wHC.
R InterPro; IPR003596; Ig_wHC.
R InterPro; IPR003596; Ig_w-
R Pfam; PF00647; Ig; 4.
R SMART; SM00407; IG; 2.
R SMART; SM00407; IGc1; 3.
R SMART; SM00406; IGv; 1.
R PR051TE; PS0085; IG_HIKE; 4.
R PR05ITE; PS00290; IG_MHC; UNKNOWN_2.
D SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;
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Best Local :
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Submitted (JUN-2004) to the
EMBL; BC073782; AAH73782.1;
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                                                                                                           PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                                                      REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
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                                                                                 PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLT
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Pred. No. 2.6e-130;
5; Mismatches 26;
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WEDLINE=2238857; PubMed=12477932;

A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Weden R.M., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., MocEwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 408
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AAH06402;
02-MAR-2004
02-MAR-2004
02-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL; BC006402; AAH06402.1; Hypothetical protein. SEQUENCE 479 AA; 52281 MP
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Mammalia; Eutheria;
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VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                     KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAP I EKT I SKAKGQPREPQ
                                                                                                                                                                                                      PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                HTEPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEFKSCDKTHTCP
                                                                                                                                                                                                                                                                                                                HTEPAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                    GQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
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                                                  KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                     PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                GOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
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Primates;
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Last sequence up
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2154.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D74E0C89082A9788 CRC64;
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No. 4.2e-130;
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RESULT
Q6MZV7
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Best Local S
Matches 401
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TISSUE-Human small intestine;
THE GERMAN HUMAN CDNA CONSORTIUM;
THE GERMAN HUMAN CDNA CONSORTIUM;
Bloecker H., Boecher M., Mewes H.W., Weil B., Ami
Pobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ dat
FROBL; BX640853; CA845920.1; -.

InterPro; IPR003109; Ig.like.
InterPro; IPR003109; Ig_like.
InterPro; IPR003109; Ig_MHC.
InterPro; IPR003597; Ig_C1.

InterPro; IPR003598; Ig_V.
Fram; PF00654; C1-set; 3.

Pfam; PF00654; C1-set; 3.

Pfam; PF0047; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00407; IGC1; 3.

PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6MZV7 PRELIMINARY; PKT; 4/3 AA.
Q6MZV7;
Q6MZV7;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence up
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation
Hypothetical protein DKFZp686C11235;
Name=DKFZp686C11235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical SEQUENCE 47
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 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
                                             EQYNSTYRVVSVLTVLHQDWLMGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                        LIGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                   LQSSGLYSLSSVVTVPSSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPB
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                                                                                        LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                   LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein.
473 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                           70.1%; Score 2152.5; DB 2; Length 473; llarity 88.3%; Pred. No. 5.5e-130; Conservative 24; Mismatches 24; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   52121 MW; 9476EAE4C0BFC447 CRC64;
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Catarrhini; Hominidae;
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 RESULT 15
BAC85444
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AC BAC85
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Best Local Similarity
Matches 401; Conserv
BAC85444
BAC85444;
02-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last seq
02-MAR-2004 (TrEMBLrel. 27, Last ann
Hypothetical protein DKFZp686C11235.
DKFZP686C11235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bloecker H., Boecher M., Mewes H.W., Weil B., Fobo G., Han M., Wiemann S.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ EMBL; BX640853; CAE45920.1; -. Hypothetical protein.
SEQUENCE 473 AA; 52121 MW; 9476EAE4COBFC44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae;
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02-MAR-2004
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                                                                                                                                                                                  SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
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 (TrEMBLrel.
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                               PRELIMINARY;
 27,
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Pred. No. 5.5e-1
24; Mismatches
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Last annotation updat
   Created)
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es 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK130844; BAC85444.1; -.
SEQUENCE 468 AA; 51224 MW; 9280ACAD6817FC20 CRC64;
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TISSUB-Thymus;

Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,

Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,

Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,

Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ27334 fis, clone TMS09201, highly similar to
C region.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammaila; Eutheria; Primata; Catarrhini; Hominidae;
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                             VFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                       LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF 243
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VFSCSVMHEALHNHYTOKSLSLSPGK
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Search completed: December Job time : 162.904 secs

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